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Database :
                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                   389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-045-673A-1
68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               May 21, 2004, 18:00:47 ; Search time 24 Seconds (without alignments) 30.115 Million cell updates/sec
Issued_Patents_AA:*
1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6. /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | 13 | 12 | 11 | 10 | 9 | 8 | 7 | 6 | ហ | 4 | ω | N | ъ. | Result No. |
|--------------------|-----------|----------------------|---------------------|--------------------|-------------------|---------------------|---------------------|-----------------|-----------------|-----------------|-------------------|------|------|-----------------|-----------------|--------------------|-------------------|--------------------|------------------|---------|-----------------|--------------------|-----------|------------------|------------------|-------------------|----------------------------|
| 35.5 | 36 | 36 | 36 | 36 | 36 | 37 | 38 | 38 | 38 | 38 | 38 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 41 | 59 | 59 | 59 | 65 | 65 | 65 | б | Score |
| 52.2 | 52.9 | 'n | 2 | 52.9 | <u>ب</u> | 54.4 | 55.9 | 55.9 | 5 | | 55.9 | 57.4 | 57.4 | 57.4 | 57.4 | 57.4 | J | 7 | \sim | 86.8 | 86.8 | ٥. | 95.6 | | 95.6 | 95.6 | % Query Match Length |
| 1504 | 970 | 402 | 256 | 250 | 98 | 65 | 749 | 556 | 556 | 556 | 556 | 695 | 507 | 496 | 496 | 115 | 99 | 82 | 898 | 474 | 474 | 458 | 458 | 458 | 94 | 89 | |
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| US-09-328-352-7046 | 5229293-2 | US-09-252-991A-20804 | US-09-134-001C-3271 | US-09-198-452A-859 | US-08-809-740A-3 | US-09-134-001C-4977 | US-09-489-039A-7979 | US-09-298-924-8 | US-09-055-210-1 | US-08-798-269-1 | US-08-505-377-1 | | 277- | US-09-291-488-2 | US-08-949-637-2 | US-08-311-731A-295 | US-08-311-731A-76 | US-08-311-731A-351 | US-09-585-858-37 | 4075 | US-08-222-619-5 | 5177002-2 | 5177002-1 | US-08-618-485B-1 | US-08-618-485B-3 | US-08-618-485B-2 | ID |
| Sequence 7046, Ap | | N | | 85 | Sequence 3, Appli | | 79 | 8, 7 | ب, | -ر | Sequence 1, Appli | 2 | 4 | N | N | 29 | 76, | 351 | 37, | ن. ب | • | Patent No. 5177002 | 5 | ,_ | u , | Sequence 2, Appli | Description |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 |
|---------------------|---------------------|--------------------|--------------------|------------------|------------------|------------------|--------------------|-----------------|---------------------|------------------|------------------|---------------------|---------------------|---------------------|-----------------|---------------------|---------------------|
| 34 | 34 | 34 | 34 | 35 | | 35 5 | | 35 | 35 | 35 | 35 | | ω 5 | ω 5 | ω G | | 35 5 |
| 50.0 | 50.0 | 50.0 | 50.0 | 51.5 | 51.5 | 51.5 | | 51.5 | | | 51.5 | | | 51.5 | | 51.5 | |
| 243 | 145 | 86 | 60 | 1531 | 1527 | 1525 | 1160 | 821 | 478 | 322 | 322 | 275 | 275 | 256 | 214 | 174 | 84 |
| 4, | 4 | 4 | 4 | 4. | 4 | 4 | 4 | _ | 4 | ຫ | щ | 4 | 4. | 4 | w | 4 | 4 |
| US-09-107-532A-4665 | US-09-134-000C-4292 | US-09-621-976-6582 | US-09-621-976-6141 | US-09-418-710-29 | US-09-418-710-27 | US-09-418-710-69 | US-09-328-352-6457 | US-08-339-578-2 | US-09-134-000C-4712 | PCT-US95-13659-2 | US-08-327-494A-2 | US-09-134-000C-6528 | US-09-107-532A-4013 | US-08-956-171E-5228 | US-09-587-066-6 | US-09-107-532A-4968 | US-09-543-681A-7825 |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| 4665, A | 4292, A | 6582, A | 6141, A | 29, App | | 69, App | | Z, Appli | 4712, Ap | 2, Appl | 2, Appli | 6528, AL | 4013, A | 5228, A | 6, Appl: | 4968, A | 7825, A |

ALIGNMENTS

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| | | ····································· |
| APPLICATION NUMBER: US 08/4/8,121 FILING DATE: 07-JUNE-1995 ATTORNEY/AGENT INFORMATION: NAME: Robert S. Silver REGISTRATION NUMBER: 35,681 REFERENCE/DOCKET NUMBER: Y1004/20002 TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 557-2010 TELEPHAX: (215) 757-1142 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 89 amino acids TYPE: amino acid TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: no ORIGINAL SOURCE: ORGANISM: Human | 4: te-3.5 inch mmpatible gc_Dos/MS-Do gc_VERSION VERSI | HONOOAAAAAAAAAA |
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US-08-618-485B-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Applic
Patent No. 6410269
                                                                                                                     TELEFAX: (215) 751-1142
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
                                                TOPOLOGY: linear
MOLECULE TYPE: pro
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                               HYPOTHETICAL: n
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Robert S. Silver
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WORDPERPECT VERSION 4.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,485B
FILING DATE: March 19, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MBDIUM TYPE: Diskette-3.5 inch, 1.44 Mb
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: Y1 TELECOMMUNICATION INFORMATION:
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DATE: December, 1985

RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103-2212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CAESAR, RIVISE, BERNSTEIN, ADDRESSEE: COHEN & POKOTILOW, LTD. STREET: 1635 Market Street, 12th Floor
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INDIVIDUAL ISOLATE:
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Serum Vitamin D-binding Protein is a Third Member
of the Albumin and Alpha Fetoprotein Gene Family
                                                                                                     amino acid
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                                                                                      linear
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                                                                                                                                                                            751-1142
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MACROPHAGE ACTIVATING FACTORS
DERIVED FROM CLONED VITAMIN D
BINDING PROTEIN AND ITS DOMAIN
AND THEIR THERAPEUTIC USAGE
FOR CANCER, HIV-INFECTION AND
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Vitamin D-binding protein
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Pred. No. 9.
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Best Local S
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/618,485B
FILING DATE: MAXCh 19, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  TELEFAX: (215) 751-114.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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AUTHORS: Cooke, Nancy E., David, E Vivek
TITLE: Serum Vitamin D-binding Protein is a Third Member
TITLE: of the Albumin and Alpha Fetoprotein Gene Family
JOURNAL: J. Clinical Investigation
VOLUME: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                  REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y:1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2010
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WORDPERFECT VERSION 4.2
CURRENT APPLICATION DATA:
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                                                    ORIGINAL SOURCE:
                                                                 MOLECULE TYPE: protein HYPOTHETICAL: no
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: CAESAR, RIVISE, BERNSTEIN, ADDRESSEE: COHEN & POKOTILOW, LTD
INDIVIDUAL ISOLATE:
                                 ORGANISM:
                                                                                                      TOPOLOGY:
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13; Conserv
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SYSTEM: PC-DOS/MS-DOS
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92.9%;
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BINDING PROTEIN AND ITS DOMAIN
AND THEIR THERAPEUTIC USAGE
FOR CANCER, HIV-INFECTION AND
OSTEOPETROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MACROPHAGE ACTIVATING FACTORS
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 Vitamin D-binding protein (Gc protein)
                                                                                                                                                                                                                                                                                                                                                                                         US/08/618,485B
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Pred. No.
                                                                                                                                                                                                                                       Y1004/20002
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418 TPKELAKLVNKRSD 431

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APPLICANT: YAMAMOTO, NOBUTO

TITLE OF INVENTION: IN VIRTO ENZYMATIC CONVERSION OF

GLYCOSLATED CHUMAN VITAMIN D BINDING PROTEIN TO A POTENT

MACROPHAGE ACTIVATING FACTOR

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION NUMBER: US/08/576,248

APPLICATION NUMBER: US/08/576,248

FILLING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 439,223

FILING DATE: 20-NOV-1989
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                                                                                                       5177002-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MACROPHAGE ACTIVATING FACTOR NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: YAMAMOTO, NOBUTO
TITLE OF INVENTION: IN VIRTO ENZYMATIC CONVERSION OF
GLYCOSLATED HUMAN VITAMIN D BINDING PROTEIN TO A POTENT
                                                                                                                                   SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 95.6%;
Best Local Similarity 92.9%;
Matches 13; Conservative
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 439,223
FILING DATE: 20-NOV-1989
O NO:1:
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                     LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 TPTELAKLVNKRSD 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                     al Similarity
13; Conserv
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Serum Vitamin D-binding Protein is a
Third Member of the Albumin and Alpha
Fetoprotein Gene Family
L: J. Clinical Investigation
TPTELAKLVNKRSE 14
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                                                            86.8%;
85.7%;
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Pred. No. 0.00056;
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Pred. No. 0.00056;
                                                            Score 59; [
Pred. No. 0.
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                                                            DB 6;
0.0071;
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US-08-222-619-5
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PCT-US95-04075-5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                            Sequence 5, Application PC/TUS95
GENERAL INFORMATION:
APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin:
TITLE OF INVENTION: Protein
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acid
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OPERATING SYSTEM: PC-DOS/MS:DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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TYPE: amino acid
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ZIP: 91320-1789
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                                                                                                                                                                                                               ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                              COUNTRY: U.S.
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85.7%;
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Pred. No.
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Best Local Similarity
"hes 7; Conserve
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US-09-585-858-37
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; ORGANISM: Bacteriophage RB69
US-09-585-858-37
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PCT-US95-04075-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic TITLE OF INVENTION: Host Organism FILE REFERENCE: 2739.1001-001 CURRENT APPLICATION NUMBER: US/09/585,858 CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: 60/137,120 PRIOR APPLICATION NUMBER: 60/137,120 PRIOR FILING DATE: 1999-06-02 NUMBER OF SEQ ID NOS: 73 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 37
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Best Local :
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APPLICANT:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                           APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
APPLICANT: NAO, JEN-I
APPLICANT: SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
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TOPOLOGY: unl
                                                                  COUNTRY:
                                                                                                                                  ADDRESSEE:
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o. 6583266
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                                                                                                     BOSTON
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Olafur H. Fridjonsson
Arnthor Aevarsson
Jakob K. Kristjansson
                                                                                  MASSACHUSETTS
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85.7%;
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: GATTES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: :
                                                                    TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: Y
ORIGINAL SOURCE:
ORGANISM: Myc
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,
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SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
STREET: 600 ATLANTIC AVENUE
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LENGTH: 82 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: Patenti
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CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                  TYPE: am:
                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                   LENGTH:
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NATI
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                  amino acid
)GY: linear
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                                                 99 amino acids
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protein
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57.1%;
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Pred. No.
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RESULT 11
US-08-311-731A-295
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                                              RESULT 12
US-08-949-637-2
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                                                                                                                                                                                                                                          US-08-311-731A-295
           Sequence 2, Application US/08949637 Patent No. 5910414
                                                                                                                                                                            Matches
                                                                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: GATES EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             MOLECULE TYPE: prot
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Mycoba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: 1
ORIGINAL SOURCE:
ORGANISM: MYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES ITTLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS ITAGENOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 600 A
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                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                            Match 57.4%; Local Similarity 57.1%;
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                                                                                                               40
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                                                                                                                                            1 TPTELAKLVNKRSE 14
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amino acid
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57.1%;
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                                                                                                                                                                                             Score 39; DB 4; Length 115; Pred. No. 7.4;
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Pred. No. 6.3;
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US-09-291-488-2
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Patent No. 6251387
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COMPUTER: IM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/949,637
FILING DATE: 14-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,370
APPLICATION NUMBER: 60/028,370
FILING DATE: 15-OCT-1996
ATTOORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 950566
TELEPHONE: 610-270-4478
TELEPHONE: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                   APPLICANT: Gwynn, Michael
APPLICANT: Kallendar, Howard
TITLE OF INVENTION: No. 6251387el Topoisomerase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,488
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                          COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 5910414el Topoisomerase I NUMBER OF SEQUENCES: 3
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STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                           STATE:
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709 Swedeland Road
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Kallendar, How
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70.0%;
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Pred. No. 37;
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CLASSIFICATION: PRIOR APPLICATION NUMBER:

08/949,637

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GENERAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Gwynn, Michael
APPLICANT: Sylvester, Daniel
APPLICANT: Katz, Lisa
APPLICANT: Warren, Richard L.
APPLICANT: Traini, Christopher M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-153-277-4
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                                                                                                                RESULT 15
US-09-153-277-2
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                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-09-153-277-4
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          Sequence 2, Application US/09153277
Patent No. 6331411
GENERAL INFORMATION:
APPLICANT: Kallender, Howard
APPLICANT: Gwynn, Michael
APPLICANT: Sylvester, Daniel
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 507
                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/153,277
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 08/949,637
EARLIER FILING DATE: 1997-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: topA FILE REFERENCE: P50566-01
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Gimmi, Edward R
REGISTRETS NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
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linear
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                                                                                                                                                                                                                                                                   Score 39; DB
Pred. No. 37;
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Pred. No. 37;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 695
TYPE: PRT
ROBANISM: Streptococcus pneumoniae
US-09-153-277-2
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                                                                Matches
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/153,277
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: 08/949,637
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                   APPLICANT: Warren, Richard L. APPLICANT: Traini, Christopher M. TITLE OF INVENTION: topA FILE REFERENCE: P50566-01
505 PTELGEIVNK 514
                                                               7;
               2 PTELAKLVNK 11
|||| ::|||
                                                               Conservative
                                                                             57.4%;
70.0%;
                                                                               Score 39; DB 4;
Pred. No. 53;
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Search completed: May 21, 2004, 18:04:17 Job time : 25 secs

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| AAG57743 | AAG57744 | ABP40132 | ABU35023 | ABG24772 | AB000788 | ABG21521 | ABB91088 | ABU28842 | ABU45138 | AAR92755 | AAR90620 | ABM68206 | ABG28629 | ABG69363 | ABG69360 | AAW97594 | AAU09101 | ABB54564 | ABU46649 |
| Aag57743 | | | | Abg24772 | Abo00788 | Abg21521 | Abb91088 | Abu28842 | Abu45138 | Aar92755 | Aar90620 | Abm68206 | Abg28629 | Abģ69363 | Abg69360 | Aaw97594 | Aau09101 | Abb54564 | Abu46649 |
| | Arabidops | Staphyloc | Protein | Novel hum | Polypept | Novel hum | Herbicida | Protein | Protein | Trehalose | Sultolobu | Photorhab | Novel hum | Babesia | Babesia | Cellulose | Novel hum | Lactococ | Protein |

| DR WPI; 2002-666885/71. | PI Schneider GB, Popoff SN, | XX PA (UYNE-) UNIV NORTHEASTERN OHIO XX | XX PR 09-NOV-2000; 2000US-0247464P. | PF 09-NOV-2001; 2001WO-US050471. | PD 01-AUG-2002. | PN WO200258589-A2. | | Modified-site | Key | OS Homo sapiens. | | | | DT 29-NOV-2002 (first entry) | | AC ABB79890; | ID ABB79890 standard; peptide; 14 AA. | RESULT 1 ABB79890 |
|-------------------------|-----------------------------|---|--|----------------------------------|-----------------|--------------------|--|---------------|---------------------|------------------|---------|---|--|------------------------------|---|--------------|---------------------------------------|----------------------|
| | SN, Safadi F; | TERN OHIO. | 247464P. | S050471. | | | /note= "glycosylated with N-acetylgalactosamine" | | Location/Qualifiers | | and any | vicamin biliaing process; therety bone; becopamin, americanticie, | Vitamin D binding protein domain III peptide fADP. | ntry) | • | | ptide; 14 AA. | |

The present peptide, designated fADP, is derived from domain III of a human vitamin D binding protein. It comprises a sugar residue, especially an N-acetylgalactosamine, attached at the Thr-3 residue, or lacks a sugar moiety. A claimed peptide for increasing bone density in a mammal comprises the first 3-13 amino acids of fADP, or has at least 70% (preferably at least 90%) homology to fADP. The peptide is used in a claimed method for promoting bone deposition. This is useful in the treatment of disorders involving bone loss, particularly osteoporosis, osteogenesis imperfecta, osteopenia, bone fracture, reconstruction of bone after tumour removal to achieve spine and other joint fusion, bone

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New peptide used for increasing bone density e.g. in treatment of osteoporosis comprises specified amino acid sequence.

Claim 1; Fig 1; 49pp; English.

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RESULT 2
AAW10562
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Matches 14
The present sequence represents the cloned domain III-derived macrophage activating factor (CdMAFI), which is from a vitamin D3 binding protein (GcP). Full length cDNA encoding the human Gc protein, isolated from a human liver cDNA library in bacteriophage lambda, was cloned into a baculovirus expression system to produce the cloned protein recombinantly. GcMAFC, CdMAF and GcMAF (similar to GcMAFC, but prepared from serum rather than recombinant protein) are used to treat cancer, or HIV, Epstein-Barr virus or herpes zoster infection, and to promote bone formation in osteoporosis. They are also adjuvants for immunisation, or vaccination. Alpha-AG is present in all patients with cancer and HIV infection, and its level is inversely correlated with precursor activity of plasma GcP, so measurement of alpha-AG may be useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloned Gc protein-macrophage activating factor; human; baculovirus; cancer; viral infection; osteoporosis; immunisation; vaccination; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW10562 standard; protein; 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        congenital, trauma induced, and oncologic restriction induced defects, in cosmetic plastic surgery, in bone-involved wound healing and related repair, in the treatment of periodontal disease and in other tooth repair processes, and in the prevention and treatment of osteoarthritis. The peptide provides regrowth of host bone and an environment to attract bone forming cells, stimulate growth of bone-forming cells, induce differentiation of progenitor bone-forming cells and supports the regeneration of the periodontal ligament and attrachment apparatus that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning vitamin D3 binding protein or its domain III in baculovirus - to produce macrophage activating factors, useful in cancer, viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 19; Fig 4; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and osteoporosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (YAMA/) YAMAMOTO N.
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96US-00618485.
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                                                                                                                        The present sequence represents the cloned domain III-derived macrophage activating factor (cdMAF2), which is from a vitamin D3 binding protein (GcP). Full length cDNA encoding the human Gc protein, isolated from a human liver cDNA library in bacteriophage lambda, was cloned into a baculovirus expression system to produce the cloned protein recombinantly. GcMAFc, CdMAF and GcMAF (similar to GcMAFc, but prepared from serum rather than recombinant protein) are used to treat cancer, or HIV, Epstein-Barr virus or herpes zoster infection, and to promote bone formation in osteoporosis. They are also adjuvants for immunisation, or vaccination. Alpha-AG is present in all patients with cancer and HIV infection, and its level is inversely correlated with precursor activity of plasma GcP, so measurement of alpha-AG may be useful for diagnosis and
                                                                                                                                                                                                                                                                                                                                                Cloning vitamin D3 binding protein or its domain III in baculovirus - produce macrophage activating factors, useful in cancer, viral infect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloned Gc protein-macrophage activating factor; human; baculovirus; cancer; viral infection; osteoporosis; immunisation; vaccination; HIV, Epstein-Barr virus; herpes zoster infection; alpha-AG.
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19-MAR-1996;
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                                                                                      Sequence
                                                                                                                                                                                                                                                                                                        Claim 20; Fig 6; 43pp; English
                                                                                                                                                                                                                                                                                                                                   and osteoporosis treatment.
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                                                                                                                               The vitamin D binding protein Gcl is an evolutionary conserved glycoprotein. Polymorphism of the Gc protein was demonstrated by gel electrophoretic analysis, which revealed two major phenotypes: Gcl and Gc2 (AAR22279). The Gc protein may be purified by a variety of means from blood, e.g. by 25-hydroxy vitamin D3-Sepharces affinity chromatography or actin-agarose affinity chromatography. Gcl may be converted to MAF by the action of glycosidases of B and T cells, e.g. by contacting Gcl in vitro with beta-galactosidase or beta-gal in combination with sialidase and/or alpha-mannosidase. The MAF may be produced in large amts. with high potency. MAF may be used for inducing macrophage activation, partic. in patients with immunodeficient diseases, cancer and other diseases characterised by impaired B- or T-cell fuction
                                                                                                                                                                                                                                                                                                                                               Prepn. of new macrophage activating factor - by contacting human gp.-specific component with glycosidase(s), useful for treating immunodeficient diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macrophage activating factor; MAF; galactosidase; sialidase; mannosidase; B cells; T cells; cancer; immunodeficient diseases; Vitamin D binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
Misc-difference 416
                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-114364/14
                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9204459-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human gp.-specific component phenotype Gcl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR22278 standard; protein; 458
                                                                                                           Sequence 458
                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                   Local
 418
                         1 TPTELAKLVNKRSE 14
                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAMAMOTO N.
TPTELAKLVNKRSD 431
                                                      Conservative
                                                                                                           A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-00576248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91WO-US006172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Asp in Gc2"
420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Gly in Gc2"
                                                                 95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Lys in Gc2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Glu in Gc2"
                                                     Score 65; DB 2;
Pred. No. 0.0013;
1; Mismatches
                                                      0
                                                                                Length 458
                                                       Indels
                                                      o
;
                                                       Gaps
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RESULT 5
AAR56975
ID AAR5

AAR56975 standard; protein; 458 AA.

Vitamin D3-binding protein GcMAFc from cloned Gc

protein.

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RESULT 6
AAW10561
ID AAW1
XX
AC AAW1
XX
AC AAW1
XX
AC Y1ta
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                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vitamin D binding protein (DBP) is converted to a macrophage activating CC factor by the action of B and T cell glycosidases. The polymorphic DBP CC phenotypes are expressed inter alia as differences in the oligosaccharide attached to the polypeptide portion of the DBP molecule. All three CC principal DBP types - DBPgm, DBPgs and DBPg differ in the nature of the papended oligosaccharide. DBPgs which possesses an oligosaccharide moiety CC which includes galactose and sialic acid residues can be converted to the CC macrophage activating factor by contact with beta-galactosidase and cc sialidase. DBBgm which is believed to possess an oligosaccharide moiety CC which includes galactose and alpha-mannose residues is contacted with beta-galactosidase and alpha-mannose residues is contacted with beta-galactosidase and cc oligosaccharide moiety which is believed to possess an oligosaccharide moiety coligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess an oligosaccharide coligosaccharide moiety which is believed to possess an oligosaccharide moiety which is believed to possess and the macrophage activating factor. The resulting factor is of high potency.
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-1989;
31-AUG-1990;
30-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vitamin D binding protein; DBP; macrophage activating factor; oligosaccharide; galactose; alpha mannose; sialic acid; beta-galactosidase; alpha-mannosidase; sialidase; MAF.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macrophage activating factor - prepared by treating glycosated vitamin D-binding protein with glycoside(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5326749-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Variant vitamin D binding protein (DBPgs/gm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
16-FEB-1995
                                                                24-SEP-1997
                                                                                                                                              AAW10561 standard; protein; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-217073/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR56975;
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                                                                                                                                                                                                                                                       418 TPTELAKLVNKRSD 431
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                                                                                                                                                                                                                                                                                    TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                            (first entry)
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(first entry)
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90US-00576248.
91US-00767742.
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                                                                                                                                                                                                                                                                                                                                                             95.6%;
                                                                                                                                                                                                                                                                                                                                                             Score 65; DB 2;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
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RESULT 7
ABP58017
ABP58017
ABP5
XX
AC ABP5
XX
DT 11-1
XX
DX
Hum
XX
Pro
KW Pro
KW dia
XX
KW Pro
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the cloned Gc protein-derived macrophage activating factor (GCMAPC), which is a vitamin D3 binding protein (GCP). Full length cDNA encoding the human Gc protein, isolated from a human liver cDNA library in bacteriophage lambda, was cloned into a baculovirus expression system to produce the cloned protein recombinantly. GCMAPC, CdMAF and GCMAF (similar to GCMAPC, but prepared from serum rather than recombinant protein) are used to treat cancer, or HIV, Epstein-Barr virus or herpes zoster infection, and to promote bone formation in osteoporrosis. They are also adjuvants for immunisation, or vaccination. Alpha-AG is present in all patients with cancer and HIV infection, and its level is inversely correlated with precursor activity of plasma GCP, so measurement of alpha-AG may be useful for diagnosis and prognosis
             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning vitamin D3 binding protein or its domain III in baculovirus - to produce macrophage activating factors, useful in cancer, viral infection and osteoporosis treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloned Gc protein-macrophage activating factor; human; baculovirus; cancer; viral infection; osteoporosis; immunisation; vaccination; HIV; Epstein-Barr virus; herpes zoster infection; alpha-AG.
                                                                                                                                                Prostate cancer; marker; vitamin D binding protein; VDBP; human; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
19-MAR-1996;
                                           Peptide
                                                                                                                     Homo sapiens.
                                                                                                                                                                                           Human serum vitamin D binding protein.
                                                                                                                                                                                                                          11-FEB-2003
                                                                                                                                                                                                                                                        ABP58017;
                                                                                                                                                                                                                                                                                    ABP58017 standard; protein; 474 AA
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                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                             418
                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                          (first entry)
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96US-00618485.
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                                                                        Location/Qualifiers 50. .65
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                               /note=
                  .94
                                                                                                                                                                                                                                                                                                                                                                                                                                     95.6%;
92.9%;
                             "marker peptide"
                                                          "marker peptide"
   "marker peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65; DB 2;
Pred. No. 0.0013;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
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                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT 8
AAR22279
ID AAR2
XX
AC AAR2
XX
DT 27-J

AAR22279 standard;

protein;

458

Å

0

27-JUL-1992 AAR22279;

(first entry)

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                                                  Matches
                                                                         Query Match
                                                                                                                       The present sequence is the protein sequence of an allele of human human serum vitamin D binding protein (VDBP). The invention provides a novel human protein that includes amino acid sequences (see ABPS805-16) that are also found in VDBP. These marker sequences can be used to distinguish VDBP-related proteins from other proteins. VDBP-related proteins are detectable at a higher concentration in serum from a mammal, e.g. a human, with prostate cancer relative to serum from a healthy mammal and can therefore be used as prostate cancer markers. They permit the rapid detection, preferably before metastases occur, of prostate cancer. A target prostate cancer-associated protein may be detected using a prostate cancer-associated proteins, and nucleic acids encoding them, are also useful as targets for treating prostate cancer, and as indicators for monitoring the efficiency of prostate cancer therapy
                                                                                                                                                                                                                                                                                                                                               Diagnosing or treating prostrate cancer by detecting in a sample isolated from the individual the presence of prostate cancer-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-067369/06.
N-PSDB; ABV76007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                  Sequence 474
                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Hlavaty J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-2001; 2001WO-US045031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MATR-) MATRITECH INC.
                                                              Local
434 TPTELAKLVNKHSD 447
                       1 TPTELAKLVNKRSE 14
                                                  12;
                                                              Similarity
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                                                Conservative
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                                                              88.2%;
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                                                1:
                                                              Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide"
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                                                               0.012;
                                                                          DB 6;
                                                                          Length 474;
                                                   Indels
                                                    0,
                                                    Gaps
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Human

gp.-specific component phenotype Gc2

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Best Local (
                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                  The vitamin D binding protein GC2 is an evolutionary conserved glycoprotein. Polymorphism of the GC protein was demonstrated by gel electrophoretic analysis, which revealed two major phenotypes: GC1 (AAR22278) and GC2. The GC protein may be purified by a variety of means from blood, e.g. by 25-hydroxy vitamin D3-Sepharose affinity chromatography or actin-agarose affinity chromatography. GC1 may be converted to MAF by the action of glycosidases of B and T cells, e.g. by contacting GC1 in vitro with beta-galactosidase or beta-gal in combination with sialidase and/or alpha-mannosidase. The MAF may be produced in large amts. with high potency. MAF may be used for inducing macrophage activation, partic. in patients with immunodeficient diseases, cancer and other diseases characterised by impaired B- or T-cell fuction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macrophage activating factor; MAP; galactosidase; sialidase; mannosidase; B cells; T cells; cancer; immunodeficient diseases; Vitamin D binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prepn. of new macrophage activating factor - by contacting human gp.-
specific component with glycosidase(s), useful for treating immuno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-114364/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deficient diseases and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9204459-A.
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Variant vitamin D binding protein (DBPg).
                         25-MAR-2003
16-FEB-1995
                                                                AAR56976;
                                                                                       AAR56976 standard; protein; 458 AA
                                                                                                                                                                                                                                                              Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YAMA/) YAMAMOTO N
                                                                                                                                                          418
                                                                                                                                                                                                          l Similarity
12; Conserv
                                                                                                                                                                                 1 TPTELAKLVNKRSE 14
                                                                                                                                                          TPKELAKLVNKRSD 431
                                                                                                                                                                                                           Conservative
                        (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-00576248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-US006172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Gly in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Lys in Gc2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Asp in Gc2"
                                                                                                                                                                                                                        86.8%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Glu in Gc2"
                                                                                                                                                                                                                        Score 59;
Pred. No.
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                         0.018;
                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                    Length 458;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                           0
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                             0
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20-NOV-1989;
31-AUG-1990;
30-SEP-1991;
                                                                                                                                                                                                                                                                                                                             Vitamin D binding protein; DBP; macrophage activating factor; oligosaccharide; galactose; alpha mannose; sialic acid; beta-galactosidase; alpha-mannosidase; sialidase; MAF.
                                                                                                                                                              Macrophage activating factor - prepared by treating glycosated vitamin binding protein with glycoside(s).
                                                                                                                                                                                       WPI; 1994-217073/26.
                                                                                                                                                                                                                                                                  04-JAN-1993;
                                                                                                                                                                                                                                                                                  05-JUL-1994.
                                                                                                                                                                                                                                                                                                US5326749-A.
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                Disclosure; Fig 2; 12pp; English.
                                                                                                                                                                                                      Yamamoto N;
                                                                                                                                                                                                                     (YAMA/) YAMAMOTO N.
                                                                                                                                                                                                                                           89US-00439223.
90US-00576248.
                                                                                                                                                                                                                                     91US-00767742
                                                                                                                                                                                                                                                                   93US-00000320
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Vitamin D binding protein (DBP) is converted to a macrophage activating CC factor by the action of B and T cell glycosidases. The polymorphic DBP CC phenotypes are expressed inter alia as differences in the oligosaccharide attached to the polypeptide portion of the DBP molecule. All three CC principal DBP types - DBPgm, DBPgs and DBPg differ in the nature of the cuppended oligosaccharide. DBPgs which possesses an oligosaccharide moiety CC which includes galactose and sialic acid residues can be converted to the CC macrophage activating factor by contact with beta-galactosidase and CC which includes galactose and slalic acid residues can be converted to the CC which includes galactose and alpha-mannose residues is contacted with beta-galactosidase and alpha-mannose residues is contacted with beta-galactose without sialic acid or cligosaccharide moiety which is believed to possess an oligosaccharide coligosaccharide moiety which is believed to possess an coligosaccharide moiety which is believed to possess an coligosaccharide moiety which is believed to possess an coligosaccharide moiety which hotudes galactose without sialic acid or coligosaccharide moiety which hotudes galactose without solid acid or coligosaccharide moiety which hotudes galactose without solid acid or coligosaccharide moiety which hotudes galactose without solid acid or coligosaccharide moiety which hotudes galactose without solid acid or coligosaccharide moiety which hotudes galactose alone to form the cc macrophage activating factor. The resulting factor is of high potency.

(Updated on 25-MAR-2003 to correct PF field.)

Sequence 458 AA;

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8
                 Matches
                         Query Match
Best Local
                        Local
                l Similarity 85.
12; Conservative
 1 TPTELAKLVNKRSE 14
                        86.8%;
85.7%;
                         Score 59;
Pred. No.
                  Mismatches
                         DB 2;
                  1;
                                 Length 458;
                   Indels
                   0
                   Gaps
                   0
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RESULT 10
AAY48469
ID AAY48
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418

TPKELAKLVNKRSD 431

AAY48469 standard; protein; 314

AAY48469;

08-DEC-1999 (first entry

Human breast tumour-associated protein 14.

Expressed sequence tag; EST; human; breast; cancer; cytostatic; medicaments; gene therapy; treatment; fat metabolism.

Homo sapiens.

DE19813835-A1

biodiversity

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RESULT 11
ABG15879
ID ABG15
XX
XX
AC ABG15
XX
DR NOVE
XX
ON Home
KW Hume
KW Hoon
XX
PN WO2
XX
PN WO2
XX
PPF 30
PF 30
XX
PF 31
PR 23
XX
PF 31
PR 23
XX
PR 24
XX
PR 24
XX
PR 25
XX
PR 25
XX
PR 26
XX
PR 27

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel human nucleic acid sequences from normal breast tissue which have cytostatic activity. The nucleic acid sequences can be used to produce and isolate full-length gene sequences. They can be used to express proteins, which can be used as tools to find an activity against breast cancer. The sequences can be used in sense or antisense form. They are especially useful for medicaments for gene therapy to treat breast cancer and for treating illnesses associated with fat metabolism. AAV48456-Y4839 represent protein fragments encoded by the expressed sequence tags described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-528979/45.
N-PSDB; AAZ33550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping;
food supplement; medical ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-2002 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human nucleic acid sequences and protein products tissue, useful for breast cancer therapy.
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                  WPI; 2001-639362/73.
N-PSDB; AAS80066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #15870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG15879 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 28; 165; 206pp;
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                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       supplement;
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                                                                                                                                                                              ΡΤ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSELRNÍVNKHSE 175
                                                                                                                                                                           Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                           2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98DE-01013835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%;
69.2%;
                                                                                                                                                                           Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g; gene mapping; gene therapy; forensic;
imaging; diagnostic; genetic disorder.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from normal breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Best Local S
Matches
                                                                                                                                                        23-APR-2001;
27-APR-2001;
05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polygeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders and partners are useful activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 46238; 103pp; English
                                                             WPI; 2003-093124/08.
                                                                                                                                                                                                                                                         23-APR-2002; 2002WO-US013142
                                                                                                                                                                                                                                                                                           31-OCT-2002.
                                                                                                                                                                                                                                                                                                                          WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                                        Fungicide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus fumigatus essential gene protein #201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABJ25543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ25543 standard; protein; 705 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                             Jiang B,
                                                                                                                             (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                          contamination;
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                                                                                                                           ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSELRNLVNKHSE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTELAKLVNKRSE 14
                                                                                             Tishkoff D,
                                                                                                                                                        ; 2001US-0285697P.
; 2001US-0287066P.
; 2001US-0295890P.
; 2001US-0303899P.
; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.7%;
                                                                                                                                                                                                                                                                                                                                                                                         essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                                                             Zamudio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44;
Pred. No.
                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                Broshkin
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                                                                                                  Lemieux
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                                                                                                  MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.

Disclosure; Page; 175pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC subject (e.g. cancer), to prevent or contain containation of an object (c) y A. funigatus, or to prevent or inhibit formation on a surface of a color binding comprising A. funigatus. The polynucleotides are useful for cc binding comprising A. funigatus. The polynucleotides are useful for cc expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. CC funigatus to identify duplicated genes or paralogues having the same or comparing the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                 05-JUN-2001;
09-JUL-2001;
31-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus fumigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention
WPI; 2003-093124/08
                                              Jiang B,
                                                                                                                                                                                                                       23-APR-2001;
27-APR-2001;
                                                                                                                                                                                                                                                                                                23-APR-2002; 2002WO-US013142.
                                                                                                                                                                                                                                                                                                                                                 31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                     WO200286090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aspergillus fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fungicide; cytostatic;
cancer; contamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus essential gene protein #801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ26143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABJ26143 standard; protein; 748 AA
                                                                                                  (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 64.: 9; Conservative
                                                                                                  ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TPADLAKLAELRSE 575
                                                 Tishkoff D,
                                                                                                                                              2001US-0285697P.
2001US-0287066P.
2001US-0295890P.
2001US-0303899P.
2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential gene; Aspergillus fumigatus; infection; biofilm; antibody; immune response.
                                                   Zamudio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB
Pred. No. 31;
1; Mismatches
                                                 ú
                                                   Broshkin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 705;
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                                                   Ξ
                                                   Lemieux SM;
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New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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Disclosure; Page; 175pp; English.

CC therapeutic use, as markers for host tissues in which the pathogenic corganisms invade or reside, for comparing with the DNA sequence of A. CC fundgatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with DNA CC sequences of other related or distant pathogenic organisms to identify optimized or other related or distant pathogenic organisms to identify CC making oligomers for attachment to a nucleic acid array for examination CC of expression patterns, for raising anti-protein antibodies, as an CC antigen to raise anti-DNA antibodies or to elicit another immune CC with which binding occurs or to identify inhibitors of the binding CC interaction. The polypeptides may be used to raise antibodies or to cellcit immune response, as a reagent in assays designed to quantitatively CC determine levels of the protein in biological fluids, as a marker for CC isolate correlative receptors or ligands in the case or virulence CC isolate correlative receptors or ligands in the case or virulence CC factors. This sequence represents a protein of one of the essential genes or content of the invention of the invention of the case or virulence CC of Aspergillus fumigatus of the invention The invention relates to novel purified or isolated nucleic acids of essential genes of Aspergillus funiquest. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic organism such as A. fumigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object by A. fumigatus, or to prevent or inhibit formation on a surface of a biofilm comprising A. fumigatus. The polymucleotides are useful for expressing recombinant protein for characterisation, screening or

Sequence 748 AA;

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             S
                               Matches
                                      Query Match
Best Local
605
              1 TPTELAKLVNKRSE 14
                                      Similarity
TPADLAKLAELRSE 618
                               Conservative
                                      63.2%;
                                     Score 43; DB
Pred. No. 33;
                               Mismatches
                                              6
                               4:
                                              Length 748;
                               Indels
                               o,
                               Gaps
                                0
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RESULT 14
AAB46728
11-SEP-2003
12-APR-2001
                                                                                                                                                       AAB46728;
                                                                                          Enterobacteria phage RB69
                                                                                                        Genome; thermophilic enzyme; washing powder; bleaching
                                                                                                                    Bacteriophage RB69 DNA polymerase protein fragment SEQ ID
                                                                              WO200075335-A2
                                                                                                                                                                   AAB46728 standard; protein; 898
                                                                                                                                  (revised)
(first entry)
```

ĕ

37

Hjorleifsdottir S,

Hreggvidsson GO,

Fridjonsson OH,

Aevarsson A;

(DECO-) DECODE GENETICS EHF.

02-JUN-1999;

99US-0137120P

02-JUN-2000; 2000WO-IB000893

14-DEC-2000.

Kristjansson JK;

in recombinant DNA technology.

Isolated nucleic acid from bacteriophage RM 378 encoding enzymes useful

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RESULT 15
ABB91986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               settings (e.g. proteases and lipases used in washing powder, hydrolytic (C enzymes used in bleaching). The isolated nucleic acid molecules and vectors are useful in the manufacture of encoded polypeptide, as probes (for isolating homologous sequences (e.g. from other bacteriophage gpecies), as well as for detecting the presence of the bacteriophage in a colture of host cells. The polypeptides can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns.

CC marker on SDS-PAGE gels or on molecular sieve gel filtration columns.

CC the enzymes and proteins of the RM378 bacteriophage is a thermophile, the enzymes and proteins of the RM378 bacteriophage are significantly comore thermostable than those of other (e.g. mesophilic) bacteriophages, such as the T4 bacteriophage of Escherichia coli. The enhanced stability come thermostable than those of other (e.g. mesophilic) bacteriophages, thus increasing the range of conditions which can be employed not only in DNA research but also in commercial settings. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel isolated nucleic molecule (I) comprising the genome of bacteriophage RM 378. The invention also describes (1) an isolated nucleic acid which encodes a polypeptide obtainable from bacteriophage RM 378, or its active derivative or fragment; (2) an isolated bacteriophage RM 378 (II); (3) a DNA construct (III) comprising operatively linked to a regulatory sequence; (4) a host cell comprising (III); and (5) an isolated polypeptide (IV) obtainable from (II), its active derivative or fragment. Bacteriophage RM 378 is useful for producing thermophilic enzymes useful in DNA research and commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 898 AA;
Identifying plant target proteins for herbicidally active compounds
                                                                                                                                                  28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                          07-FEB-2002
                                                                                                                                                                                                                                                               WO200210210-A2.
                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                  Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                     Herbicidally active polypeptide SEQ ID NO 1197.
                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB91986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB91986 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3A-P; 42pp; English.
                                      WPI; 2002-269010/31.
                                                                         Tietjen K,
                                                                                                                                                                                     28-AUG-2001; 2001WO-EP009892
                                                                                                              (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTEITKVFNQRKE 484
                                                                         Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
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                                                                                                                 Matches
                                                      Query Match
Best Local S
                                                                                                                                                                The invention relates to identifying target proteins (ABB90790-ABB4016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                       comprising aligning and from plant with nucleic organisms.
                                                                                                                 Sequence 1124 AA;
                                                                                                                                                                                                                                                                                                                                      Claim 5; SEQ ID NO 1197; 261pp + Sequence Listing; English.
2 PTELAKLVN 10
                                     Similarity
8; Conserv
                                       Conservative
                                                        58.8%;
                                                                                                                                                                                                                                                                                                                                                                                           comparing nucleic acid or amino acid sequences acid or amino acid sequences from non-plant
                                       <u>,</u>
                                                        Score 40; DB 5;
Pred. No. 1.9e+02;
                                           Mismatches
                                                                          Length 1124;
                                           0
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Search completed: May 21, 2004, 18:01:52 Job time : 57 secs

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486 PTELCKLVN 494

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Result
No.
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                Score
                                      Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/IS06 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/IS06 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/US09B PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/US09C PUBCOMB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/US09C PUBCOMB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/US10A PUBCOMB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

15: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

17: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

19: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

17: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

18: /cgn2 6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*
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68
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                                                                                                                                                                                                                                                                                                Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                              Length DB
   14
94
458
474
474
705
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898
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                 15 US-10-045-673A-1
US-09-826-463-2
US-09-826-463-1
US-09-826-463-1
US-09-826-463-1
US-09-98-909-14
US-10-128-714-3201
US-10-128-714-8201
US-10-270-786-37
US-10-270-875-37
US-10-270-875-37
US-10-270-878-37
US-10-270-786-37
US-10-270-710-37
                                                                                                                                                                                                                                                                                                IJ
                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Sequence 1, Appli
GENERAL INFORMA
GENERAL INFORMA
GENERAL INFORMA
Sequence 14, Appl
Sequence 34177, A
Sequence 3201, Ap
Sequence 20429, A
Sequence 196, App
Sequence 196, App
Sequence 37, Appl
                                                                                                                                                                                                                                                                                              Description
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 |
|-------------------|------------------|-----|----------------------|-----|------------------|------|---------|----------|----------------------|-------------------|---------------------|----------|----------------------|-----------|---------------------|----------|--------|--------------------|------------------|------------------|-------------|------|----------------------|--------------|-----------|------|----------------|-------------------|-------------------|
| 36 | 36 | 36 | 36 | 36 | 36 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 41 |
| 52.9 | •' | | | | | 54.4 | • | 54.4 | • | 54.4 | 54.4 | | | 55.9 | ٠ | ٠ | | | | • | • | • | 57.4 | ٠ | • | • | 57.4 | • | 60.3 |
| 250 | 212 | 178 | 79 | 62 | 51 | 1820 | 1820 | 1230 | 692 | 588 | 506 | 493 | 1946 | 1750 | 729 | 729 | 711 | 327 | 259 | 216 | 151 | 1161 | 1029 | 865 | 710 | 709 | 701 | 61 | 898 |
| 15 | 12 | 12 | 12 | H | 12 | 15 | 15 | 14 | 12 | 14 | 15 | 12 | 12 | 12 | 15 | 12 | 12 | 5 | 14 | 14 | 9 | 15 | 12 | 12 | 15 | 12 | 12 | 14 | 14 |
| -10-289-762- | -10-424-59 | 110 | US-10-424-599-192519 | -40 | -10-424-599-1641 | 9-49 | 69-493- | 3-524- | US-10-282-122A-60918 | 3- | US-10-108-260A-4387 | -10-425- | US-10-282-122A-62947 | Ļ | US-10-369-493-23632 | 0-282-13 | 0-282- | US-10-369-493-3029 | US-10-234-432-31 | US-10-234-432-28 | 9-969-384-2 | | US-10-424-599-245114 | -10-425-114- | -10-369-4 | -10- | -10-282-122A-7 | -10-097- | US-10-270-846-37 |
| Sequence 859, App | Sequence 230315, | æ | e 192519, | ø | e 164190 | æ | O. | e 6, Apr | æ | Sequence 6, Appli | æ | e 57893, | e 62947 | e 920, Ap | | e 56 | 73 | e 3029 | e 31 | e 28 | 22, | 36 | Sequence 245114, | 5576 | e 18415, | Ø | 74009, | Sequence 397, App | Sequence 37, Appl |

ALIGNMENTS

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US-10-045-673A-1
US-10-045-673A-1
US-10-045-673A-1
Sequence 1, Application US/10045673A
PADLICATION NO. US20030229014A1
PADLICANT: Depoif, Steven N
APPLICANT: Schmeider, Gary B
APPLICANT: Schmeider, Gary B
APPLICANT: Sefadi, Fayez
TITLE OF INVENTION. Agents and Methods for Promoting Bone Growth
FILE REFERENCE: 25080/04000
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US/10/045,673A
CURRENT FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
INVEST: 14
PRIOR FILING DATE: 2001-11-09
INVEST: 14
INVEST: 15-05; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
APPLICATION:
APPLICANT: NOBUTO YAMAMOTO
INVENTION: PREPARATION OF POTENT
TITLE OF INVENTION: PREPARATION OF POTENT
TITLE OF INVENTION: PREPARATION OF POTENT
THE OF INVENTION: PREPARATION OF POTENT
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THE OF INVENTION: DERIVED FROM CLONED VITAMIN D
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US-09-826-463-2
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                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-3.5 inch, 1.44

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT VERSION 4.2

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DATE: December, 1985
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 4 and 5
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:

NAME: Robert S. Silver
REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y1004/20002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2010
TELEPAX: (215) 751-1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/826,463
FILING DATE: 05-Apr-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/08/618,485B
                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PREPARATION OF POTENT
MACROPHAGE ACTIVATING FACTORS
DERIVED FROM CLONED VITAMIN D
BINDING PROTEIN AND ITS DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NOBUTO YAMAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TPTELAKLVNKRSE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CAESAR, RIVISE, BERNSTEIN,
COHEN & POKOTILOW, LTD.
STREET: 1635 Market Street, 12th Floor
                                                                                                                                                                                                                                           ADDRESSEE: CAESAR, RIVISE, BEI
COHEN & POKOTILOW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: March 19, 1996
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-JUNE-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                     STREET: 1635 Market Street,
                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                  CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL:
APPLICATION NUMBER: US/09/826,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                               PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2420-2424
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Pred. No. 0.00041;
1; Mismatches 0
                                                                                                                                                                                                                                                            BERNSTEIN,
                                                                                                                                                                                                                       12th Floor
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US-09-826-463-1
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APPLICANT: NOBUTO YAMAMOTO

TITLE OF INVENTION: PREPARA
                                                                                                APPLICATION NUMBER: US/09/826,463
FILING DATE: 05-Apr-2001
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US/08/618,485B
FILING DATE: March 19, 1996
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-70UB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Robert S. $11Ver
REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y1004/20002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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DATE: December, 1985

RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 10 TO 94
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/618,485B
FILING DATE: March 19, 1996
APPLICATION NUMBER: US 08/478,121
FILING DATE: 07-UNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT VERSION 4.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103-2212
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                         JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215)
JOURNAL: J. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,681
REFERENCE/DOCKET NUMBER: Y1004/20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-Apr-2001
                                                           TELEPHONE: (215) 567-2010
TELEPAX: (215) 751-1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1635 Market Street, 12th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CAESAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 567-2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Robert S. Silver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (215) 751-1142
J. Clinical Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAESAR, RIVISE, BERNSTEIN, COHEN & POKOTILOW, LTD.
                                               Clinical Investigation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACROPHAGE ACTIVATING FACTORS DERIVED FROM CLONED VITAMIN D BINDING PROTEIN AND ITS DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PREPARATION OF POTENT
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Pred. No. 0.00043
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Query Match Best Local S Matches 13

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                                                    OTHER INFORMATION: MAP TO AJ009613.3
OTHER INFORMATION: EXPRESSED IN LUNG
OTHER INFORMATION: EXPRESSED IN PLACI
OTHER INFORMATION: SWISSPROT HIT: QU
US-10-029-386-34172
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; ORGANISM: Homo sapiens
US-09-998-909-14
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34172, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence
SEQ ID NO 34172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 12; Conserv
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Patent No. US20020164664A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 92.9
Matches 13; Conservative
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Best Local Similarity
                  Query Match
                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hlavaty, John
APPLICANT: Briggman, Joseph
TITLE OF INVENTION: Detection and Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                             FEATURE:
                                                                                                                                                                                                ENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: December, 1985
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1-485
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 TPTELAKLVNKHSD 447
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85.7%;
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64.7%;
69.2%;
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                                                                     IN LUNG, SIGNAL = 0.87
IN PLACENTA, SIGNAL =
HIT: Q04279, EVALUE 2.
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Pred. No. 0.0025;
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Pred. No. 0.021;
 Score 44;
Pred. No.
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   DB 14;
1.7;
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2.10e+00
                  Length 58;
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US-10-128-714-8201
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            FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8603
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3201
LENGTH: 705
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                                                                                                                                                                                                                                                                                                                                                                                                              Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8201, Application US/10128714 Publication No. US20030119013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                       APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamuddo, Carlos
APPLICANT: Zamuddo, Carlos
APPLICANT: Zamuddo, Carlos
APPLICANT: Lemieux, Sebastien M
APPLICANT: Lemieux, Sebastien M
TITLE OP INVENTION: Identification of Essential Genes in Aspergillus fumigatus of TITLE OP INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 10182-018-99
FULNE APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-3
PRIOR FILING DATE: 2001-04-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/295,890 PRIOR FILING DATE: 2001-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/303,899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           562 TPADLAKLABLRSE 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTELAKLVNKRSE 14
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NUMBER: US 60/303,899
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Pred. No.
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Query Match
Best Local Similarity
"herhes 9; Conserve
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US-10-128-714-8201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-401-403-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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SEQ ID NO 8201
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 196, Application US/10401403
Publication No. US20040005599A1
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SEQ ID NO 20429
SOFTWARE: Pat
SEQ ID NO 196
LENGTH: 856
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
ENTERED OF TABLE OF THE PROPERTY OF 
                                                                                                     APPLICANT: Schoenbrunner, Nancy
APPLICANT: Myere, Thomas
APPLICANT: Myere, Thomas
APPLICANT: Gelfand, David
TITLE OF INVENTION: THERMOSTABLE OR THERMOACTIVE DNA POLYMERASE MOLECULES
TITLE OF INVENTION: WITH ATTENUATED 3'-5' EXONUCLEASE ACTIVITY
FILE REFERENCE: 21314-USI
CURRENT APPLICATION NUMBER: US/10/401,403
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US 60/369,815
PRIOR FILING DATE: 2003-04-02
NUMBER OF SEQ ID NOS: 203
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PRIOR APPLICATION NUMBER: US 60/316,362
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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ublication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TELAKLVNKRS 13
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                                                                     PatentIn version 3.2
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Pred. No. 34;
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APPLICANT: Gudmundur O. Hreggyidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Jakob K. Kristjansson
APPLICANT: Jakob K. Kristjansson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT APPLICATION NUMBER: US/09/585,858
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 898
TYPE: PRT
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US-10-401-403-196
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US-10-270-875-37
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TYPE: PRT
; ORGANISM: Bacteriophage RB69
US-10-270-875-37
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PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
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Best Local Similarity
Matches 7; Conserv
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ORGANISM: Bacteriophage RB69
-10-270-878-37
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APPLICANT: Gudmundur O. Hreggvidse
APPLICANT: Olafur H. Fridjonsson
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CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
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APPLICANT: Jakob K. Kristjanson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
TITLE OF INVENTION: 1001-001
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Olafur H. Fridjonsson
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
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; ORGANISM: Bacteriophage RB69
US-10-270-786-37
                                        US-10-270-710-37
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Best Local Similarity 55...
7; Conservative
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                                                                                                                        SEQ ID NO 37
Query Match
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/270,710
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-12-18
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APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
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APPLICANT: Gudmundur O. Hreggvidss
APPLICANT: Olafur H. Fridjonsson
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APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sigridur Hjorleifsdotter
                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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                                                           LENGTH: 898
TYPE: PRT
ORGANISM: Bacteriophage RB69
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Olafur H. Fridjonsson
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No. US20030087392A1
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Olafur H. Fridjonsson
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  60.3%; Score 41; DB 14; Length 898;
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Search completed: May 21, 2004, 18:05:12 Job time: 43 secs
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US-10-270-859-37
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SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 898
TYPE: PRT
ORGANISM: Bacteriophage RB69
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                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/270,859
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR PILING DATE: 1999-06-02
NUMBER: 007-17-18-1999-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidss
APPLICANT: Olafur H. Fridjonsson
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Olafur H. Fridjonsson
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                       Query
Match Length DB
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Gapop 10.0 , Gapext 0.5
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68
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1: pir1:*
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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alpha-amylase (EC fatty oxidation co fatty avidation co fatty avid beta ox hypothetical prote hypothetical prote large (alpha) chai lactose operon replactose phosphotra conserved hypothet sqdx protein (U453 hypothetical prote
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| 4 4 5 | 4.3 | 4 4 2 1 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
|--|--------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 | 37 |
| 54.4 54.4 | 54.4 | 54.4 4.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 | 54.4 |
| 1210 | 819 | 692 | 644 | 644 | 543 | 540 | 540 | 540 | 539 | 448 | 369 | 365 | 364 |
| NN | | N 1 | | N | | | N | | | | | | N |
| A53183 | A82549 | AI1596 | T47835 | A36325 | A46601 | A98174 | S47708 | A86020 | A84534 | F84780 | T50820 | AF2893 | S26458 |
| pnage-related pro- epidermal growth f | | DNA topoisomerase | hypothetical proce | epidermal growth i | sarafotoxin precur | hypothetical prote | hypothetical 61.2K | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | glycosyltransferas | hypothetical prote |

| R;Braun, A Biochim. B A;Title: S; A;Referenc: A;Accessio: A;Status: 1 A;Molecule A;Residues | A, Title: Serum vital A, Title: Serum vital A, Reference number: A, Accession: A92765 A, Molecule type: mRM A, Residues: 1-167,' A, Cross-references: A, Experimental source A, Experimental source | A;Reference number: A;Accession: A29096 A;Status: translatio: A;Molecule type: DNA A;Residues: 1-19 <ym a;cooke,="" a;cross-references:="" david<="" n.e.;="" td=""><td>A;Molecule A;Residues A;Cross-re; A;Experimes R;Yang, F. Gene 54, 2) A;Title: Ti</td><td>A; restance A; Cross-re A; Experime R; Witke, W Genomics 11 A; Title: C A; Title: C A; A; Ceessio A; A; Status: 1</td><td>RESULT 1 VYHUD Vitamin D-) N;Alternat C;Species: C;Date: 28 C;Accessio R;Yang, F. Proc. Natl A;Title: H A;Title: H A;Molecule</td><td>وب بن در حرب در حرب</td><td></td></ym> | A;Molecule A;Residues A;Cross-re; A;Experimes R;Yang, F. Gene 54, 2) A;Title: Ti | A; restance A; Cross-re A; Experime R; Witke, W Genomics 11 A; Title: C A; Title: C A; A; Ceessio A; A; Status: 1 | RESULT 1 VYHUD Vitamin D-) N;Alternat C;Species: C;Date: 28 C;Accessio R;Yang, F. Proc. Natl A;Title: H A;Title: H A;Molecule | وب بن در حرب در حرب | |
|--|--|---|---|--|--|---------------------------|---|
| Braun, A.; Kofler, A.; Morawietz, S.; Braun, A.; Kofler, A.; Morawietz, S.; Hochim. Biophys. Acta 1216, 385-394, Title: Sequence and organization of Reference number: S39787; MUID:94092, Accession: S39787, Accession: S39787, Status: preliminary, Molecule type: DNA, Molecule type: DNA, Residues: 1-431, 'E', 433-435, 'T', 437- | erum vitamin e number: A9 n: A92765 type: mRNA type: mRNA ferences: GB | n: A29096 n: A29096 translation n type: DNA : 1-19 <yan2> : 1-15 GB: .E.; David, A</yan2> | type: DNA: 1-431,'E', ferences: GB ferences: GB ntal source: Naberhaus, 85-290, 1987 he vitamin D | A;Restoues: 1-4/4 CIAMIA A;Cross-references: GB:X03178; GB:M11321 A;Experimental source: allele Gc2 A;Experimental source: allele Gc2 A;Experimental source: 2 Installed Gc2 A;Fitte: W.F.; Gibbs, P.E.M.; Zielinski, Genomics 16, 751-754, 1993 A;Title: Complete structure of the human A;Reference number: A46759; MUID:9331517 A;Accession: A46759 A;Status: nucleic acid sequence not shown | binding prote names DBP Homo sapien Homo sapien Homo sapien 1, 24076; A. J. L. Acad. Sci. May 1709-8 e number: A9 n. A94076 type: mRNA. | | |
| .; Moraw 1216, 3 organiza 9787; MU | D-bindi 2765; MU 2765; MU 169-326, :M12654; allele | 9096; MU not show > :M17156; E.V. | 433-435, :L10641; allele K.H.; A | :X03178; allele p.E.M.; 1993 cture of 6759; MU sequenc | ein prec ; Gc-glo s (man) equence 46759; A .; Naylo U.S.A. pecific 4076; MU | | 0 C C A C C C C C C C C C C C C C C C C |
| Ribraun, A.; Kofler, A.; Morawietz, S.; Cleve, H. Rijchim. Biophys. Acta 1216, 385-394, 1993 Aritle: Sequence and organization of the human vitamin A; Factoric number: S39787; MUID:94092730; PMID:7505619 A; Accession: S39787 A; Status: preliminary A; Status: Symptomic Status A; Status: Symptomic Status A; Status: Symptomic Status A; Status | A;Tille: Serum vitamin D-binding protein is A;Reference number: A92765; MUID:86086396; Pl A;Reference number: A92765; MUID:86086396; Pl A;Accession: A92765 A;Accession: A92765 A;Rosidues: 1-167,'E',169-326,'R',328-431,'E A;Residues: 1-167,'E',169-326,'R',328-431,'E A;Residues: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1646,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481; A;Cross-references: GB:M1654,'C',109:181481,'C', | n NID:g181489; | A; Molecule type: DNA A; Residues: 1-431, 'E', 433-435, 'T', 437-474 <wit> A; Residues: 1-431, 'E', 433-435, 'NID: g340281; PID! A; Cross-references: GB: L10641; NID: g340281; PID! A; Experimental source: allele Gc1 R; Yang, F:, Naberhaus, K.H.; Adrian, G.S.; Garde Gene 54, 285-290, 1987 A; Title: The vitamin D-binding protein gene contacts.</wit> | A; Kesloues: 1-4/4 (IAMIA) A; Cross-references: GB:X03178; GB:M11321; NID:g31675; PIDN A; Experimental source: allele Gc2 A; Experimental source: allele Gc2 A; Experimental source: allele Gc2 A; Witke, W.F.; Gibbs, P.E.W.; Zielinski, R.; Yang, F.; Bow Genomics 16, 751-754, 1993 A; Title: Complete structure of the human Gc gene: differen A; Title: Complete structure of the human Gc gene: differen A; Reference number: A46759; MUID:93315171; PMID:8325650 A; Accession: A46759 A; Status: nucleic acid sequence not shown; translation not | RESULT 1 VYHUD VYHUD Vitamin D-binding protein precursor [validated] Vitamin D-binding protein precursor [validated] Vilernate names: DBP; GC-globulin; group-spec C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence revision 28-May-1 C;Accession: A94076; A46759; A29096; A32765; S2765; A32765; S3 R;Yang, F; Brune, J.L.; Naylor, S.L.; Cupples, proc. Natl. Acad. Sci. U.S.A. 82, 7994-7998, 19 A;Title: Human group-specific component (Ge) is A;Reference number: A94076; MUID:86068030; PMID A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA | | AF2893 2 T50820 2 T50820 2 T80820 2 R84780 2 R86020 2 R947708 2 A98174 2 A98174 2 A46601 2 A36325 2 T17835 2 T17835 2 A11596 |
| leve, H. human vitamin D-binding protein PMID:7505619 <bra></bra> | A;Title: Serum vitamin D-binding protein is a third member of the albumin A;Reference number: A92765; MUID:86086396; PMID:2416779 A;Reference number: A92765; MUID:86086396; PMID:2416779 A;Accession: A92765 A;Accession: A92765 A;Residues: 1-167,'E',169-326,'R',328-431,'E',433-435,'T',437-474 <cco>A;Residues: 1-167,'E',169-326,'R',328-431,'E',433-435,'T',437-474 <cco>A;Residues: 1-167,'E',169-326,'R',328-431,'E',433-435,'T',437-474 <cco>A;Cross-references: GB:M1654,'RDI:g181481; PIDN:AAAS2173.1; PID:g181482 A;Experimental source: allele Gcl</cco></cco></cco> | MID:2958390 PIDN:AAA19662.1; PID:g46309 | WIT> PIDN:AAA61704.1; PID:g639896 Gardella, J.M.; Brissenden, J.E.; contains conserved nucleotide se | g31675; PIDN:CAA26938. 'ang, F.; Bowman, B.H.; ne: differences and sin D:8325650 nslation not shown | human ific component 986 #text_change 9787, A24066; A9 R.L.; Naberhaus 85 85 a member of the :2415977 | epidermal pridermal | glycosyltransferas glycosyltransferas hypothetical prote sarafotoxin precur epidermal growth f hypothetical prote bunk topoisomerase DNA topoisomerase phage-related protections are protected protections. |
| ein gene. | min and alpha fet | 9 | 96 J.E.; Bowman, B.l ide sequences tha: | 1; PID:g31676 Dugaiczyk, A. milarities between | 17-Mar-2000 9427; A03237 , K.H.; Bowman, B.H. albumin family | | nsferass I prote precur Precur I prote merase merase |

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A; Molecule type: protein
A; Residues: 17,'Q',19-21,'N',23-36,'XXX',40-41;472-474 <SVA>
C; Comment: DBP is a multifunctional protein found in plasma, ascitic fluid, cerebrospina nts polymerization of actin by binding its monomers. DBP associates with membrane-bound C; Comment: Over 80 variants of human DBP have been identified. The three most common all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S67480; NID:g455967; PIDN:AAB29423.1; PID:g455970
R;Schoentgen, F.; Metz-Boutigue, M.H.; Jolles, J.; Constans, J.; Jolles, P.
Biochim. Biophys. Acta 871, 198-198, 1986
A;Title: Complete amino acid sequence of human vitamin D-binding protein (group-specifi A;Reference number: A24066; MUID:86216223; PMID:2423133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Liu, J.; Yu, K.; Chen, H.; Weng, S.
Biochem. Biophys. Res. Commun. 219, 868-875, 1996
Biochem. Biophys. Res. Commun. 219, 868-875, 1996
A;Title: Regulatory region with putA gene of proline dehydrogenase that links
A;Reference number: JC4661; MUID:96216743; PMID:8645272
A;Accession: JC4661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: putA protein
C;Species: Photobacterium leiogr
C;Date: 10-Sep-1999 #sequence_re
C;Accession: JC4661
멍
                                                                                                                                                                                                                                                                                                                     A;Gene: putA
C;Superfamily: proline dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: C; Comment: This enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U39227; NID:g1236800; PIDN:AAC43866.1; PID:g1236801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-314 <LIU>
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A;Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3;
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Reywords: actin binding; duplication; globulin; glycoprotein; liver; plasma; polymorph;
Reywords: signal sequence #status predicted <SIG>
11-474/product: vitamin D-binding protein (allele Gc2) #status experimental <MAL2>
11-431, E', 433-435, T', 437-474/Product: vitamin D-binding protein (allele Gc1) #status;
26-199/Domain: serum albumin repeat homology <SA1>
1217-385/Domain: serum albumin repeat homology <SA2>
1240-474/Domain: serum albumin repeat homology <SA3>
1240-474/Domain: serum albumin repeat homology <SA3>
1240-474/Domain: serum albumin repeat homology *SA3>
1240-474/Domain: serum albumin repe
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iochemistry 18, 1611-1617, 1979
;Title: Molecular basis for the three major forms of human serum vitamin D binding Reference number: A90427; MUID:79145448; PMID:218624
;Accession: A90427
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enzyme is a multifunctional
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Pred. No.
2; Mismatc
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Pred. No. 0.013;
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Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliter
A;Reference number: AD3252; PMID:11756688
A;Greens AF3445
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BY Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium All Reference number: AB1807; MUID:21595285; PMID:11759840
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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AF3445
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A;Residues: 1-248 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72317.1; PID:g17129704; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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A;Gene: alr0359
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A;Residues: 1-392 <KUR>
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                                                                                                                                                                                   Gene: BMEI1548
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                                                                                                     58.8%;
77.8%;
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Pred. No. 11;
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#text_change 09-Dec-
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unknown protein F22H5.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A96783
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Maiti, E.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.A.; Liu, Z.A.; Liu, Z

Kaul, S.; White, R.; Creasy, T.H.;

O.; Alonso ; Dewar, K

Khaykin, E.; Kim, (Maiti, R.; Marzial)

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A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A96783
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A;Molecule type: DNA
A;Residues: 1-626 <STO>
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R;anonymous, The C: elegans Sequencing Consortium.
R;anonymous, The C: elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Rote: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C_elegans/ published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein Y49E10.11 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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A;Molecule type: DNA
A;Residues: 1-593 <STO>
                                                                                                                                                                                                                                                                                              probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: B84742
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                     A;Molecule type: DNA
A;Residues: 1-1124 <STO>
A;Cross-references: GB:AE002093; NID:g2924777; PIDN:AAC04906.1; GSPDB:GN00139
                                                                                                                        A; Reference number: A84420;
A; Accession: B84742
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;Gene: Y49E10.11
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Genetics
                                                                                                Status: preliminary
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Pred. No.
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Pred. No.
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                                                                                                                                                      me 2 of the plant Arabidopsis thaliana PMID:10617197
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C.Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1998
A;Reference number: Z22831
A;Accession: T44732
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T44732
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                                                                                                                A;Cross-references: EMBL:X75356; NID:g407370; PIDN:CAA53109.1; PID:g407377 C;Superfamily: Coxiella burnetii hypothetical protein 117
                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 117 - Coxiella burnetii
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A;Experimental source: cosmid B1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein MLCB1450.16 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-117 < THI>
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A; Residues: 1-117 <WIL>
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                                                                                                                                                                                                                                                                                                    A; Reference number: S52227
                                                                                                                                                                                                                                                                                                                     R; Willems, H.; Thiele, D.; Valkova, submitted to the EMBL Data Library,
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A;Residues: 1-71 <JAM>
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                                                                                                                                                                                                                                                                                                                                                  Species: Coxiella burnetii
Date: 05-May-1995 #sequence_revision 01-Sep-1995;Accession: $52233; $38221
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Pred. No.
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Pred. No. 12;
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hypothetical protein F55C5.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t

#sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

RESULT 10

T22716

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C;Accession: D98014

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcza R;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, E.J.; Lu, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zoc A;Title: Genome of the Bacterium Streptococcus pneumc A;Reference number: A97872; MUID:21429245; PMID:1154; A;Accession: D98014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, Capitle: Complete Genome Sequence of a virulent isolate A;Reference number: A95000; MUID:21357209; PMID:11463916 A;Accession: F95146
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A;Molecule type: DNA
A;Residues: 1-699 <KUR>
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A;Residue: 1-622 <WIL>
A;Cross-references: EMBL:Z78198; PIDN:CAB01573.1; GSPDB:GN00023; CESP:F55C5.8
A;Experimental source: clone F55C5
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A;Accession: T22716
A;Status: preliminary; translated from
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C; Superfamily:
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A;Experimental source: strain TIGR4
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                                                                                                                                                                                                                               DNA topoisomerase (EC 5.99.1.2) [imported] - Streptococcus pneumoniae (strain C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
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A;Reference number: Z19604
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              Molecule type: DNA
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1-701 <KUR
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76;
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E.J.; Lu, J.; Matsushima
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Streptococcus
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Radune, D.; Holtzapple,
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                        C;Genetics:
                                           A; Contents: annotation
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A;Gene: topA
C;Superfamily: DNA topoisomerase
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C;Genetics:
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10.4 < KUR>
A;Residues: 1-10.4 < KUR>
A;Residues: 1-10.4 < KUR>
A;Cross-references: GB:AB006469; PIDN:AAK64659.1; PID:g14523056; GSPDB:GN00165
A;Cross-reference number: A96039; MUID:21368234; PMID:11474104
A;Reference number: A96039; MUID:21368234; PMID:11474104
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A;Residues: 1-710 <STO>
A;Cross-references: GB:AE005176; PID:g12724201; PIDN:AAK05328.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium A;Reference number: A99262; MUID:21396509; PMID:11481432
A;Accession: A95262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable formate dehydrogenase (EC 1.2.1.2) alpha chain FdoG [imported] - Sinorhizobium C;Species: Sinorhizobium meliloti
C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA topoisomerase (EC 5.99.1.2) [imported] - Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Species: Lactococcus lactis subsp. lactis ;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Superfamily: DNA topoisomerase I
;Keywords: isomerase; phosphotransferase
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7; Conserva
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70.0%;
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Pred. No.
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No.
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RESULT 15
T17866
T17866
T17866
C; Species: Chlorella virus PBCV-1
C; Species: Chlorella virus PBCV-1
C; Species: Chlorella virus PBCV-1
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T17866
R; Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A; Reference number: Z18806
A; Retaus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-255 <GRA>
A; Residues: 1-255 <GRA>
A; Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96734.1
A; Experimental source: specific host Chlorella strain NC64A
C; Genetics:
A; Note: A366L
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C;Superfamily: formate dehydrogenase
C;Keywords: oxidoreductase
Search completed: May 21, 2004, 18:03:41 Job time: 23 secs
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                                                                                                   226 PTELKKIVGKFEE 238
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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Gapop 10.0 , Gapext 0.5
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68
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  SwissProt_42:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                     543
606
1210
1230
181
184
247
247
250
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903
557
710
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351
351
364
 SRIX_ATREN
ABD4 MOUSE
EGRE_MOUSE
ST20 CANAL
YCZ2_YEAST
RRF_THETN
NP24_LYCES
OS81_SOLCO
GPEE_CHLPN
3MGA_BACSU
OTC_LACPL
OTC_ASPNG
                                                                                                                            FADB_ECOLI
FADB_SALTI
FADB_SALTI
FADB_SALTI
FADB_SALTI
FADB_SALTY
RRF_WIGBR
LACR_STAAM
LACR_STAAM
ECRL_METTH
MATK_SAXOP
CD6V_METTF
CD6Z_METTF
VTDB_RABITI
YHIJ_ECOLI
YHIJ_ECOLI
                                                                                                                                                                                                                                                            VIDB HUMAN
DPOL BPR69
RUVB RALSO
TP6B PYRAE
SR68 CAEEL
TOP1 LACLA
TMM MYCPE
FPRB MYCLE
FADB_ECO57
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 OBewb6 mycoplasma
O3304 mycobacteri
Q8x812 e fatty oxi
P21177 e fatty oxi
P21177 e fatty oxi
Q8236 s fatty oxi
Q8236 s fatty oxi
Q8255 wiggleswort
Q99873 staphylococ
P16644 staphylococ
P16649 methanobact
Q33134 saxifraga o
P29570 methanobact
P29570 methanobact
P29570 methanobact
P37627 staphylococ
P37627 escherichia
P13208 attractaphis
O80212 candida alb
P3066 saccharomyc
Q8ra24 thermoanaer
P12670 lycopersico
P50702 solanum com
Q927a2 chlamydia p
P37873 bacillus
P11066 aspergillus
                                                                                                                                                                                                                                                                     Q38087 bacteriopha
Q89236 ralstonia s
Q89236 pyrobaculum
Q20822 caenorhabdi
Q9c980 lactococcus
Q8ewb6 mycoplasma
Q33064 mycoplateri
                                                                                                                                                                                                                                                                                                                                      P02774 homo sapien
Q38087 bacteriopha
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staphylococ
d staphylococ
d staphylococ
o methanobact
d saxifraga o
methanobact
o methanobact
o myctolagus
d secherichia
d atractaspis
d mus musculu
g mus musculu
g mus musculu
c candida alb
b saccharomyc
d thermoanaer
o lycopersico
solanum com
c chlamydia p
b acillus su
lactobacill
s aspergillus
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 |
|--------------------|--------------------|--------------------|--------------------|------------|--------------------|------------|--------------------|------------|--------------------|------------|------------|
| 35 | 35 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 |
| 51.5 | 51.5 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 | 52.9 |
| 181 | 149 | 3432 | 3432 | 3432 | 1440 | 1048 | 978 | 888 | 654 | 544 | 453 |
| | ᆫ | Н | Н | H | Н | μ | ь | -ب | ᆫ | Н | ب |
| Y06E_BPT4 | RL9_FUSNN | POLG JAEVJ | POLG_JAEVS | POLG_JAEV1 | POLG_JAEVN | NMD5 YEAST | SIR3_YEAST | YJHO_YEAST | RPC3_YEAST | SYFB SULSO | NH12_CAEEL |
| P13311 bacteriopha | Q8ril0 fusobacteri | P32886 j genome po | P19110 j genome po | j genome | P14403 j genome po | Ö | P06701 saccharomyc | | P32349 saccharomyc | | ٠. |

ALIGNMENTS

| RA RA | RA R | R R R R R R R R R R R R R R R R R R R | OS RA | RESULT VIDB H ID V AC P DT 2: DT 1: DT 1: DE V GN GG |
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| אחשות ותיים | "Boutique MH., Jolles d sequence of human vit gronent: evidence of a malbumin and alpha-fet cta 871:189-198(1986). ND 431-441. "ubMed=218624; | SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=86086396; PubMed=2416779; Cooke N.E., David E.V.; Cooke N.E., David E.V.; "Serum vitamin D-binding protein is a third member of the albumin and alpha feroprotein gene family."; J. Clin. Invest. 76:2420-2424(1985). [3] SEQUENCE FROM N.A. MEDLINE=94092730; PubMed=7505619; MEDLINE=94092730; PubMed=7505619; Braun A., Kofler A., Morawietz S., Cleve H.; "Sequence and organization of the human vitamin D-binding protein gene."; gene."; Biochim. Biophys. Acta 1216:385-394(1993). | Homo sapiens (Human). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI TaxID=9606; SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=86068030; PubMed=2415977; Yang F., Brune J.L., Naylor S.L., Cupples R.L., Naberhaus K.H., Bowman B.H.; "Human group-specific component (Gc) is a member of the albumin family "; family "; Proc. Natl. Acad. Sci. U.S.A. 82:7994-7998 (1985). | HUMAN STANDARD; PRT; 474 AA. VIDB HUMAN STANDARD; PRT; 474 AA. P02774; Q16309; Q16310; 21-UUL-1986 (Rel. 01, Created) 21-UUL-1986 (Rel. 01, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Vicamin D-binding protein precursor (DBP) (Group-specific component) (GC-globulin) (VDB). |

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EMBL; L10641; AAA61704.1; -.
EMBL; X03178; CAAA6938.1; -.
EMBL; X03178; CAAA6938.1; -.
EMBL; M12654; AAA52173.1; -.
EMBL; S67480; AAB29423.1; JOINED.
EMBL; S67474; AAB29423.1; JOINED.
EMBL; S67476; AAB29423.1; JOINED.
EMBL; S67479; AAB29423.1; JOINED.
EMBL; S67479; AAB29423.1; JOINED.
EMBL; S67479; AAB29423.1; JOINED.
EMBL; S67526; AAB29423.1; JOINED.
EMBL; S67526; AAAB29423.1; JOINED.
EMBL; S77129; AAA19662.2; -.
EMBL; S77129; AAA19662.2; -.
EMBL; S77129; AAA19625.1; ALT_SEQ.
EMBL; S77129; AAD14250.1; ALT_SEQ.
                                                                                                                  PIR; A94076; VYHUD.
PDB; 1J78; 06-FEB-02.
PDB; 1J78; 06-FEB-02.
PDB; 1KW2; 19-JUN-02.
PDB; 1KXP; 19-JUN-02.
PDB; 1LOT; 31-JUL-02.
PDB; 1MA9; 11-FEB-03.
GlycoSuiteDB; P02774; -
SWISS-2DPAGE; P02774; -
Siena-2DPAGE; P02774; -
Genew; HGNC:4187; GC.
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Braun A., Bichlmaier R., Cleve H.;
"Molecular analysis of the gene for the human vitamin-D-binding protein (group-specific component); allelic differences of the genetic GC types.";
Hum Cont 'A'
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between
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HIS-445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95242701; PubMed=7725672;
Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
"Characterization of mutants of the vitamin-D-binding protein/group
specific component: GC aborigine (1A1) from Australian aborigines and
South African blacks, and 2A9 from south Germany.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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modified and this statement
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"The vitamin
GO; GO:0005386; F:carrier activity; TAS. GO; GO:0005499; F:vitamin D binding; TAS. GO; GO:0015875; P:vitamin/cofactor transport; InterPro; IPR000264; Serum_albumin. Pfam; PF00273; transport_prot; 2. PRINTS; PR00802; SERUMALBUMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerebrospinal fluid, and urine and on the surface of many cell types. In plasma, it carries the vitamin D sterols and prevents polymerization of actin by binding its monomers. DBP associates with membrane-bound immunoglobulin on the surface of b-lymphocytes and with IgG fc receptor on the membranes of T-lymphocytes. SUBCELLULAR LOCATION: Secreted.

POLYMORPHISM: Over 80 variants of human DBP have been identified. POLYMORPHISM: Common alleles are called GC*1F, GC*1S, and GC*2. The three most common alleles are called GC*1F, GC*1S, and GC*2. SIMILARITY: Belongs to the ALB/AFP/VDB family.

SIMILARITY: Contains 3 albumin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sang. 68:50-54(1995).
FUNCTION: Multifunctional protein found in plasma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet.
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AC Q38087;
AC Q38087;
DT 15-UUL-1998
DT 10-OCT-2003
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MEDLINE=96064739; PubMe
Wang C.C., Yeh L.-S., K
"Modular organization o
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SMART; SM00103; ALBUMIN; 2
PROSITE; PS00212; ALBUMIN;
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                 MEDLINE=97358535; PubMed=9215631; Wang J., Sattar A.K., Wang C.C., Steitz T.A.;
                                                                                                            phylogenetics.";
J. Biol. Chem. 2
                                                                                                                                                                                                                                        Bacteriophage RB69.
Viruses; dsDNA viruses,
T4-like viruses.
TG1 TaxID=12353;
                                                                                                                                                                                                                                                                                                                                          DNA polymerase
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"Crystal structure of
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-7 Т.А.;
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SM00103; ALBUMIN; 2.
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36, Last sequence
42, Last anno
3C 2.7.7.7) (Gr
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of T4 DNA polymerase.
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7) (Gp43).
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E -> R (IN REF. 2).
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Pred. No. 0.0053;
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R -> C (in allele GC*2A9).

/FTId=VAR 014120.

R -> H (in allele GC*1A1; dbSNP:222038).
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                                     Karam J.D.,
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InterPro; IPRO06172; DNA_pol_B.
InterPro; IPRO06134; DNA_pol_B_exo.
InterPro; IPRO06133; DNA_pol_B_exo.
Pfam; PF00136; DNA_pol_B; 1.
Pfam; PF00136; DNA_pol_B exo; 1.
PKINTS; PR00106; DNA_pol_B.
SMART; SM00486; POLBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U34036; AAA93077.1; -.
PDB; 1WAL; 14-JAN-98.
PDB; 1WAL; 14-JAN-98.
PDB; 1CLQ; 28-OCT-99.
PDB; 1E1F; 29-DEC-99.
PDB; 1E8H; 05-NOV-99.
PDB; 11G9; 11-JUN-01.
PDB; 11H7; 13-JUN-01.
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                                                                                                                                                                                                                                                                                                             PROSITE; PS00116; DNA POLYMERASE B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
Exonuclease; DNA-binding; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20004392; PubMed=10535734;
Shamoo Y., Steltz T.A.;
"Building a replisome from interacting pieces:
complexed to a peptide from DNA polymerase and
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89:1087-1099(1997).
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RESULT 3
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Q8Y236;
28-FEB-2003
                                                                                                                                                                                                                                             MEDLINE=21681879; PubMed=11823852; Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange Nandler M., Choisne N., Chandler M., Schlex T., Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schlex T., Gaspin C., Thebault P., Whalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Holliday junction DNA helicase ruvB.
RUVB OR RSC0500 OR RSC5022.
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                                                                                                             -I- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures cruciform structure in supercoiled DNA with palindromic sequence, indicating that it may promote strand exchange reactions in homologous recombination. RuvAB is an helicase that mediates the Holliday junction migration by localized denaturation and reanneling (By similarity).

--- SUBUNIT: Forms a complex with ruvA (By similarity).
--- SUBUNIT: Belongs to the ruvB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TURN
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                      NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
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EMBL; AL646059; CAD14028.1;
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Pred. No. 18;
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(See http://www.isb-sib.ch/announce/
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RESULT 4
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Best Local
HAMAP; MF_00322; -; 1.
InterPro; IPR003594; ANTPbind ATPase.
InterPro; IPR005734; DNA_top6B.
Pfam; PF02518; HATPase_c; 1.
SMART; SM00387; HATPase_c; 1.
TIGRPAMS; TIGR01052; top6b; 1.
Isomerase; Topoisomerase; DNA-binding; SEQUENCE 527 AA; 59870 MW; 7BAADBB
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SEQUENCE
                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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InterPro; IPR003553; AAA_ATPase_centr.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR004605; RuvB_C.
InterPro; IPR008823; RuvB_C.
InterPro; IPR008824; RuvB_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRAE
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE PROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. NP_BIND 73
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                                                                                                                                                                                                                                                                                                                                                                    Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type II DNA
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                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the hyperthermophilic crenarchaeon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003
                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoi of double-stranded DNA.
SUBUNIT: Heterotetramer of two subunits A and two subunits B
                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Relaxes
                                                                                                                                                                                                                                                                                                                                       exhibits a strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 TPTELARIVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00004; AAA; 1.
PF05491; RuvB_C; 1.
PF05496; RuvB_N; 1.
                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A. 99:984-989(2002).
UNCTION: Relaxes both positive and negativ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00382; AAA; 1.
18; TIGR00635; ruvB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPTELAKLVNK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
topoisomerase VI subunit B (EC 5.99.1.3) (TopoVI-B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Created)
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39058 MW;
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                                                                                                                                                                                                                                                                                                                                        decatenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoprotei; Thermoproteales;
  DNA-binding; ATP-binding; Co
MW; 7BAADB81F8FC9D97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB Pred. No. 11; 3; Mismatches
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47795DB5F7AD7DC6 CRC64;
                                                                                                                                                                                                                                                                                                                                       ive and negative activity. The B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       527
                                                                                                                                                      (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                           Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                            passage and rejoining
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subunit binds
                  Complete
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                  proteome.
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Best Local
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Q20822;
16-OCT-2001
              16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                 LACLA
                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                           PIR; T22716; T22716.
WormPep; F55C5.8; CE20875.
InterPro; IPR008941; TPR-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CABEL
                                                      TOP1_LACLA
Q9CGB0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                               Hypothetical protein; Signal RNA-binding.
                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Harris B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F55C5.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probable signal recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                          Local Similarity
-OCT-2001 (Rel. 4
-OCT-2001 (Rel. 4
-FEB-2003 (Rel. 4
A topoisomerase I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       participate in the elongation arrest function (By similarity).
SUBUNIT: Signal recognition particle consists of a 75 RNA molecule
of 300 nucleotides and six protein subunits: SRP72, SRP68, SRP54,
SRP19, SRP14 and SRP9 (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to the SRP68 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Signal-recognition-particle assembly has a crucial role in targeting secretory proteins to the rough endoplasmic reticulum membrane. SRP68 binds the 7S RNA, SRP72 binds to this complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subsequently. This ribonucleoprotein complex might interact directly with the docking protein in the ER membrane and possibly
                                                                                                                                        499
                                                                                                                                                                                                                                                                                                                                    Z78198; CAB01573.1;
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                                                                                                                                                                TPTELAKLVNKR 12
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                                                                                                                                                                                                                                                    622
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nilarity 57.1%;
Conservative
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                    A.
                                                                    STANDARD;
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40, Created)
40, Last sequence update)
41, Last annotation update)
I (EC 5.99.1.2) (Omega-prot
                                                                                                                                                                                                                                                    70574 MW;
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                                                                                                                                                                                                          57.4%;
58.3%;
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Last annotation update)
nition particle 68 kDa protein (SRP68).
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Pred.
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Pred. No. 29;
                                                                                                                                                                                                                                                                              recognition particle; Ribonucleoprotein;
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                    A7B8808E46169636 CRC64;
                                                                                                                                                                                             Mismatches
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(Omega-protein)
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16;
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                                                                                                                                                                                            1;
                                                                                                                                                                                                                       Length 622;
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 (Relaxing enzyme)
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                        8
                                                       Best Loc
Matches
                                                                                   Query Match
                                                                                                                                                                                                                                                 Pfam; PF01131; Topoisom bac; 1.
Pfam; PF0175; Toprim; 1.
Pfam; PF0136; Zf-C4 Topoisom; 3.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1Ac; 1.
SMART; SM00436; TOP1BG; 1.
SMART; SM00493; TOPRIM; 1.
                                                                                                              ZN FING
ZN FING
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ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

    -I- FUNCTION: The reaction catalyzed by topoisomerases leads to the
conversion of one topological isomer of DNA to another.
    -I- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lactis ssp. lactis II1403.";
Genome Res. 11:731-753(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bolotin A., Wincker P., Mauger Weissenbach J., Ehrlich S.D.,
                                                                                                                                                                                                                     TIGRFAMS; TIGR01051; topA_bact; 1.
PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005733;
InterPro; IPR000380;
InterPro; IPR003601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Untwisting enzyme)
                                                                                                                                                                                          Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P06612; 1ECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE006355; AAK05328.1; PIR; F86778; F86778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006154;
                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003602;
InterPro; IPR006171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp.
                                                                                                                                                                                                       somerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence of the lactic acid bacterium Lactococcus
                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA, followed by passage and rejoining.
SUBUNIT: Monomer (By similarity).
MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
backbone bond, it simultaneously forms a protein-DNA link, in
which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
at one end of the enzyme-severed DNA strand.
SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family.
518
                           N
                                                                                                                                                                                       Complete proteome.
                                                       Similarity 7; Conserv
PTELGEIVNK
                           PTELAKLVNK 11
                                                                                                                                                                                                       Topoisomerase; DNA-binding;
                                                                                                                710 AA;
                                                                                                                                             595
635
676
                                                        Conservative
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663
702
321
527
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DNA_tpisomrase.
DNAtopI_ATP_bind.
DNAtopI_DNA_bind.
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                                                                                                                   80741
                                                                      57.4%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                      Toprim_sub.
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Toprim_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ibsp. lactis) (Streptococcus lactis).
Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauger S
                                                                                                                   ¥.
                                                        2
                                                        Score 39; DB Pred. No. 34; 2; Mismatches
                                                                                                              C4-TYPE 1.
C4-TYPE 2.
C4-TYPE 3 (ATYPICAL).
DNA CLEAVAGE (BY SIMILARITY).
; 1268E706C38A59EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorokin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaillon O., Malarme
                                                                                                                                                                                                       Zinc-finger; Metal-binding;
                                                                                    1;
                                                                                    Length 710;
                                                           Indels
                                                          0
                                                           Gaps
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TRMB_MYCPE
ID TRMB_M
AC Q8EWB6

TRMB_MYCPE Q8EWB6;

STANDARD;

PRT;

220

RESULT 7

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FPRB
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Best Local (
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HAVAD; MF 01057; -; 1.

InterPro; IPR004395; Cons hypoth91.

InterPro; IPR004395; Methyltransf_4.

Pfam; PF02390; Methyltransf 4; 1.

TIGRPAMs; TIGR00091; TIGR00091; 1.

TIGRPAMs; TIGR00091; TIGR00091; 1.

Transferase; Methyltransferase; tRNA processing; Complete proteome.

Transferase; Methyltransferase; TRNA processing; Complete proteome.

25888 MW; FFA0D7E5F19DA310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITINE=22354719; PubMed=12466555;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Fur Sasaki Y., Ishikawa J., Shiba T., Sasaki T., Hattori M.;
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
The complete genomic sequence of Mycoplasma penetrans, an intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002)
-i- FUNCTION: Catalyzes the formation of N(7)-methylguanine at position 46 (m7946) in tRNA, (By similarity).
-i- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-ade homocysteine + tRNA containing N(7)-methylguanine.
-i- SIMILARITY: Belongs to the methyltransferase superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003
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10-OCT-2003
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Bacteria; Firmicutes;
NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tRNA
MBDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Ha
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Mo
                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Create 28-FEB-2003 (Rel. 41, Last s 10-OCT-2003 (Rel. 42, Last a Probable ferredoxin/ferredox FPRB OR MLZ134 OR MLCB57.39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry
                                                                                                                                                                               NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                      033064;
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                        Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                           FPRB_MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collak ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for content of the statement is not removed.
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CT-2003 (Rel. 4

CT-2003 (Rel. 4

(guanine-N(7))
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42, Last sequence update)
42, Last annotation update)
-)-methyltransferase (EC 2.
                                                                                                                                                                                                        Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                      ferredoxin--NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.9%;
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                                                                                                                                                                                                                                                                                                                                                     Created)
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Pred. No.
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                                                                                                                                                                                                          Mycobacterium
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16;
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                                                                                  N.R.,
        Hamlin N.,
Moule S.,
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Enterobacteriaceae; Escherichia.

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FADB ECO57
Q8X8I2;
28-FEB-2003
                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fatty oxidation complex alpha subunit [Includes: Encyl-CoA hydratase (EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-encyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR OLDB OR Z5367 OR ECS4774.

BECherichia coli O157:H7.
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SEQUENCE
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InterPro; IPR001450; 4Fe48 ferredoxin.
InterPro; IPR000813; 7Fe ferredoxin.
InterPro; IPR000759; Adrndx_reductase.
InterPro; IPR001337; FAD pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Nature 409:1007-1011(2001).
-i- CATALYTIC ACTIVITY: Reduced ferredoxin + N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murphy L., Oliver K., Quail M.A., Rutter S., Seeger K., Simon S., Si Squares S., Stevens K., Taylor K.,
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PRINTS; PR00354; 7FESFRDOXIN.
PRINTS; PR00419; ADXEDTASE.
PRINTS; PR00368; FADPNR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z99494; CAB16679.1; -. EMBL; AL583924; CAC31089.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: FAD; probably binds
-!- SIMILARITY: In the N-terminal,
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Barrell B.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00198; 4FE4S FERREDOXIN; 1. Oxidoreductase; Flavoprotein; NADP; FAI Iron-sulfur; 4Fe-4S; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T45351; T45351.
HSSP; P55907; 1XBR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ferredoxin family.
SIMILARITY: IN THE C-TERMINAL,
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72.78;
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2 (4FE-45) (BY SIMI
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the bacterial-type
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S., Woodward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.A., Rutherford
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SEQUENCE FROM N.A STRAIN=0157:H7 / I

NCBI_TaxID=83334;

MEDLINE=21074935; PubMed=11206551;

EDL933 / ATCC 700927;

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354 TEAAKLLNKQLE 365

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Best Local &
                                   Matches
                                                                                                                                                                                   InterPro; IPR006180; 3HCDH.
InterPro; IPR006108; 3HCDH C.
InterPro; IPR006108; 3HCDH N.
InterPro; IPR006176; 3HCDH C_1ike.
InterPro; IPR001927; 6DGDH C_1ike.
InterPro; IPR001753; EnCoA_hydrtse.
Pfam; PF00725; 3HCDH N; 1.
Pfam; PF002737; 3HCDH N; 1.
Pfam; PF002737; 3HCDH N; 1.
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).

-I- FUNCTION: FadB and fadA are the alpha and beta subunits of the multifunctional enzyme complex of the fatty acid degradation cycle (By similarity).

-I- CATALYTIC ACTIVITY: (S)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kirk S., Bouttin A., Bohay Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                    Lyase; I
                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long. As its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                 PROSITE; PS00067; 3HCDH; 1.

PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.

Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase;
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Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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                                                                                                                                                                                                                                                                                                                               PIR; F91225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: In the N-terminal section; belongs to the hydroxyacyl-CoA dehydrogenase family. SIMILARITY: In the C-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hydroxybutancyl-CoA.

CATALYTIC ACTIVITY: 3-cis-dodecencyl-CoA = 2-trans-dodecencyl-CoA.

PATHMAY: Fatty acid beta-oxidation cycle; third step.

SUBUNIT: Tetramer of two alpha chains and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: (3S)-3-hydroxyacyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: (S)-3-hydroxybutanoyl-CoA = (R)-3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydratase/isomerase family.
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                                                                                                                                                                                                                                                                                                                                             AE005615; AAG59040.1;
AP002567; BAB38197.1;
                                                                                                    Isomerase; Complete
CE 729 AA; 79559 M
w
                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                s requires a license agreement (See an email to license@isb-sib.ch).
                                   Conservative
                                                  55.9%;
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                                                                                                    proteome.
MW; C13EBBFFFA749183
                                  Score 38; DB
Pred. No. 52;
2; Mismatches
                                   2
                                                  DB
52;
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                                                                    Length 729;
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                                   Indels
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Tobe T.,
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01-AUG-1992 (Rel. 23, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fatty oxidation complex alpha subunit [Includes: Enoyl-CoA hydro
(EC 4.2.1.17), Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase
(EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-
bydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR OLDB OR B3846.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FADB
This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use, by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                           Yang X.Y.H., Schulz H., Elzinga M., Yang S.Y.;
"Nucleotide sequence of the promoter and fadB gene operon and primary structure of the multifunctional oxidation protein from Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary sequence of the Escherichia coli fadBA operon, encoding the fatty acid-oxidizing multienzyme complex, indicates a high degree of homology to eucaryotic enzymes."; J. Bacteriol. 172:6459-6468 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91035260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daniels D.L., Plunkett G. III "Analysis of the Escherichia from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12 / MG1655;
MEDLINE=92358234; PubMed=1379743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINB=90370500;
Nakahigashi K., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacherichia coli
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91291827;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of the fadA and fadB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
                                                                                             hydroxybutanoyl-CoA.

CATALYTIC ACTIVITY: 3-cis-dodecenoyl-CoA = 2-trans-dodecenoyl-CoA.

PATHWAY: Fatty acid beta-oxidation cycle; second step.

SUBUNIT: Tetramer of two alpha chains and two beta chains.

SIMILARITY: In the N-terminal section; belongs to the 3-hydroxyacyl-CoA dehydrogenase family.

SIMILARITY: In the C-terminal section; belongs to the enoyl-CoA
                                                                                                                                                                                                                CATALYTIC ACTIVITY:
COA + H(2)O.
                                                                                                                                                                                                                                                  cycle.
catalytic Activity: (s)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
                                                                                   hydratase/isomerase family.
                                                                                                                                                                                                    CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                              + NADH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K., Inokuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        PubMed=1712230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=1699931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2204034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia.
                                                                                                                                                                                                   (S) -3-hydroxybutanoyl-CoA = (R) -3-
                                                                                                                                                                                                                               (3S) - 3 - hydroxyacyl - CoA =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coli
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acid
                                                           a collaboration
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RESULT 11
FADB_SALTI
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EMBL; X52837; CAB40809.1; -.
EMBL; M59368; AAA23750.1; -.
EMBL; M14164; AAA62777.1; -.
PIR; A39592; A39592.
HSSP; P00348: 3HPH
                                                                MEDLINE=11534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain (Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fatty oxidation complex alpha subunit [Includes: Enoyl-CoA hydratase (EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR STY3577; OR T3315.
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CONFLICT
CONFLICT
CONFLICT
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Pfam; PF02737; 3HCDH N; 1.

Pfam; PF02737; 3HCDH N; 1.

Pfam; PF00378; ECH; 1.

PROSITE; PS00067; 3HCDH; 1.

PROSITE; PS00166; ENOYL COA HYDRATASE; 1.

Fatty acid metabolism; MultIfunctional enzyme; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006180; 3HCDH.
InterPro; IPR006108; 3HCDH C.
InterPro; IPR006176; 3HCDH N.
InterPro; IPR008927; 6DGDH_C_11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P00348; 3HDH.
ECO2DBASE; G073.4; 6TH
ECO2DBASE; G073.5; 6TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8Z3C6;
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CT18;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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  SEQUENCE FROM N.A. STRAIN=Ty2 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae;
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729 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ceria; Gammaproteobacteria;
Salmonella.
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F -> L (IN REF.
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-> L (IN REF. 2).
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6F1055E402F6B129 CRC64;
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RESULT
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                                                ZO-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Fatty oxidation complex alpha subunit [Includes: Enoyl-CoA hydratase (EC 4.2.1.17); Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8); 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35); 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)].
FADB OR STM3983 OR STMD1.6.
Salmonella typhimurium
Bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR006180; 3HCDH. C.
InterPro; IPR006180; 3HCDH C.
InterPro; IPR006176; 3HCDH N.
InterPro; IPR006176; 3HCDH N.
InterPro; IPR001753; EnCoA_hydrtse.
Pfam; PF007725; 3HCDH, 2.
Pfam; PF002737; 3HCDH, 1.
Pfam; PF002737; 3HCDH, 1.
Pfam; PF00378; ECH; 1.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
PAGE MILLIFORM MULTIFUNCTIONAL en.
Lyase; Isomerase; Complete proteome.
SEQUENCE 729 AA; 79642 MW; C34C68ECFF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage hy content entitles requires a license agrance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22531367; PubMe Deng W., Liou S.-R., Pl Burland V., Kodoyianni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
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EMBL; AE016845; AAO70843.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY:
                        Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Tetramer of two alpha similarity). SIMILARITY: In the N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hydroxybutanoyl-CoA.
CATALYTIC ACTIVITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Fatty acid
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y: 3-cis-dodecenoyl-CoA = 2-trans-dodecenoyl-CoA.
id beta-oxidation cycle; third step.
of two alpha chains and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                             365
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RESULT 13

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Matches 8
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InterPro; IPRO06180; 3HCDH C.
InterPro; IPRO06176; 3HCDH N.
InterPro; IPRO06176; 3HCDH N.
InterPro; IPRO01753; EnCoA_hydrtse.
InterPro; IPRO01753; EnCoA_hydrtse.
InterPro; IPRO01753; EnCoA_hydrtse.
InterPro; IPRO01753; EnCOH, 1.
Pfam; PF00778; 3HCDH N; 1.
Pfam; PF00378; ECH; 1.
PROSITE; PS00166; ENOYL COA HYDRATASE; 1.
FROSITE; PS00166; ENOYL COA HYDRATASE; 1.
FRATLY ACID metabolism; Multifunctional en
Lyase; Isomerase; Complete proteome.
SEQUENCE 729 AA; 79594 MW; 90A6EAB578
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF233324; AAF33409.1;
EMBL; AE008886; AAL22827.1;
StyGene; SG?????; fadB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Leonard S., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LT2 / SGSC1412 / ATCC / VV / 2
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P00348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinforma
Buropean Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: 3-cis-dodecenoyl-CoA = 2-trans-dodecenoyl-CoA. PATHWAY: Fatty acid beta-oxidation cycle; third step. SUBUNIT: Tetramer of two alpha chains and two beta chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY:
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CATALYTIC ACTIVITY: (
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SIMILARITY: In the C-terminal
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                                                                                                                                                                                  TELAKLVNKRSE 14
   (Rel. 42, Created)
(Rel. 42, Last sequence update)
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cycling factor (Ribosome releasing
                                                                                                                                                                                                                 Conservative
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SGSC1412 / ATCC 700720;
                                                                             STANDARD;
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                                                                                                                                                                                                                               55.9%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complex
                                                                                                                                                                                                                 Score 38; DB Pred. No. 52; 2; Mismatches
                                                                             PRT;
                                                                                                                                                                                                                                                                              90A6EAB57871582D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            section; belongs to the enoyl-CoA
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of the
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52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                           enzyme; Oxidoreductase;
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A SEQUENCE FROM N.A.

A SEQUENCE FROM N.A.

RESTAIN=MASO / ATCC 700699, and N315;

RX MEDLINE=21311952; PubMed=11418146;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shi

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RESULT 14
LACR_STAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aksoy S.;
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Wigglesworthia glossinidia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACR STAAM STANDARD; PRT; 251 AA (299873; 15-MAR-2004 (Rel. 43, Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probom; PD004103; RRF; 1.
TIGRFAMs; TIGR00456; frr; 1.
Protein biosynthesis; Complete
SEQUENCE 185 AA; 21650 MW;
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HAMAP; MF_00040; -; 1.
InterPro; IPR002661; RRF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=158878, 158879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
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Pred. No. 20;
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C71569E7155DECFD CRC64;
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Kaito C.,
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RESULT 15
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Matches
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Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LACR_ST;
P16644;
                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratewen the Swiss Institute of Bioinformatics and the EMBL outstations on the European Bioinformatics Institute. There are no restrictions on
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-!- SIMILARITY: BELONGS TO THE DEOR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
DNA BIND 20
SEQUENCE 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001034; HTH DeoR.
InterPro; IPR009058; Wing_hlx_DNA_bnd.
Pfam; PF00455; deoR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP003364; BAB58358.1; -.
EMBL; AP003136; BAB43288.1; -.
PIR; G90015; G90015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS;
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                                                                                                                                                                                                                                                                                                         MEDLINE=90299802; PubMed=2163387;
                                                                                                                                                                                                                                                                                                                                              STRAIN=RN4220
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus aureus (strain MW2), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactose phosphotransferase system LACR OR MW2122.
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PROSITE; PS00894; HTH_DEOR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactose metabolism; Transcription regulation; Repressor; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ancet 359:1819-1827(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 AA;
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28593 MW;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-T-H MOTIF (BY SIMILARITY).
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It is produced through a collaboration
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                                                                                                                                                                                                                                           EMBL; AP004829; BAB95987.1; -.
EMBL; M32103; AAA67854.1; -.
PIR; A44506, A44506.
                                                                                                                 Complete proteome.
DNA_BIND 20
SEQUENCE 251 AA;
                                                                                                                                                         PRINTS; PR00037; HTHLACR.
SMART; SM00420; HTH DEOR; 1.
PROSITE; PS00894; HTH DEOR FAMILY; 1.
Lactose metabolism; Transcription regulation; Repressor; DNA-binding;
                                                                                                                                                                                                                   InterPro; IPR001034; HTH_DeoR.
Pfam; PF00455; deoR; 1.
                                                   Similarity 7; Conserv
             ELAKLVNKR 12
EIAKLVNKK 17
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251 AA;
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                                                                                                                 39 H
28549 MW;
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Search completed: May 21, Job time : 13 secs 2004, 18:02:16

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Maximum DB seq
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Q8YZU6
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Q7WL59
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Q7VWG8
Q87440
Q8YFH4
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          Q93p54 vibrio sp.
Q51873 photobacter
Q9uns2 homo sapien
Q89e44 bradyrhizob
Q7zvt8 brachydanio
Q8yzu6 anabaena sp
Q8d9i0 vibrio vuln
Q87c79 xylella fas
Q7w7s2 bordetella
Q7w7s2 bordetella
Q7w9s8 bordetella
Q7w9s8 bordetella
Q8yfh4 brucella me
Q8g2e5 brucella su
Q9ff17 arabidopsis
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A Asgeireson B., Andresson O.S.;

It Asserts structure of cold-adapted alkaline phosphatase from a Vibrio pp., as deduced from the nucleotide sequence.";

Biochim. Biophys. Acta 0:0-0(2001).

EMBL; AP52014; AAX94204.1; -.

R GO; GO:0008152; P:metabolism; IEA.

InterPro; IPR001952; Alk phosphtse.

Pfam; PF00245; alk phosphtse.

Pfam; PF00245; alk phosphtse; 1.

PRINTS; PR00113; ALKPHHTASE.

R PROSITE; PR00113; ALKPPC; 1.

R PROSITE; PS00123; ALKALINE PHOSPHATASE; 1.

SEQUENCE 521 AA; 57384 NW; 0DC4930D4D9CF192 CRC64;
                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           Q93P54
Q93P54;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                   Alkaline phosphatase.
Vibrio sp. G15-21.
Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=169049;
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                         TPTELAKLVNKRSE 14
 TPEKLABIVNKNSB 416
                                                      Conservative
                                                               69.1%;
                                                                                                                                                                                                                                                                                                                                                                  Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                  Score 47; I
Pred. No. 5.
                                                      Mismatches
                                                                  DB 2;
5.8;
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                                                                                 Length 521;
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RESULT 2

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01-NOV-1996
01-JUN-2003
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BIR; JC4661; JC4661.

GO; GO:0004657; F:proline dehydrogenase activity;
GO; GO:0006537; P:glutamate biosynthesis; IEA.
GO; GO:0006562; P:proline catabolism; IEA.
InterPro; IPR002872; Pro_dh.
Pfam; PP01619; Pro_dh; 1.

NON TER
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35213 MW; 6E85DBCE8E225BB7 CF
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Q51873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UNS2; O43191;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
COP9 complex subunit 3 (COP9 (Constitutive PHOTOMORPHOGENIC,
ARABIDOPSIS, homolog) subunit 3) (JAB1-containing signalosome subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin J.W., Yu K.Y., Chen H.Y., Weng S.F.;
"Regulatory region with putA gene of proline dehydrogenase that links to the lum and the lux operons in Photobacterium leiognathi.";
Biochem. Biophys. Res. Commun. 219:868-875(1996).
EMBL; U39227; AAC43866.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTA.
Photobacterium leiognathi.
                                                                                                                                                                                                                                 MEDLINE-99206679; PubMed=10191102; Potocki L., Chen K.-S., Lupski J.R.; "Subunit 3 of the COP9 signal transduction complex plants to humans and maps within the smith-magenis region in 17p11.2."; Genomics 57:180-182(1999).
                                                                                                                                                                                                                       Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COPS3 OR SGN3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gam
Vibrionaceae; Photobacterium.
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MEDLINE=98194867; PubMed=9535219; Seeger M., Kraft R., Ferrell K., Schade R., Gordon C., Naumann M.,
                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                         Submitted
                                                                                                                                             Strausberg R.;
                                                                          SEQUENCE OF 21-423 FROM N.A.
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                                                                                                                         EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Dubiel W.;
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Best Local S
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Best Local
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FASEB J. 12:469-478 (1998).
EMBL; AF098109; AAD41247.1; -.
EMBL; AF008191; AAD41247.1; -.
EMBL; AF031647; AAC14197.1; -.
Genew; HGNC:2239; COPS3.
GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0009716; P:response to light; TAS.
GO; GO:000717; PCI.
InterPro; IPRO00717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
Q7ZVT8;
Q7ZVT8;
01-JUN-2003
01-JUN-2003
01-QCT-2003
Similar to C
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Q89E44;
01-JUN-2003
01-JUN-2003
01-OCT-2003
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SEQUENCE
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MEDLING=22484998; PubMed=12597275;
MEDLING=22484998; PubMed=12597275;
MEDLING=22484998; PubMed=12597275;
Mancho T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Sasamoto S., Watanabe A., Shimpo S., Tsuruoka H., Wada T., Yamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genomic sequence of nitrogen-fixing Bradyrhizobium japonicum USDA110."; DNA Res. 9:189-197(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bradyrhizobium japonicum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP005961; BAC52508.1; -. GO; GO:0006118; P:electron transport; InterPro; IPR001128; Cytochrome_P450. Pfam; PF00067; p450; 1.
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SE 423 AA; 47873 MW;
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                                    (TrEMBLrel. 24, (TrEMBLrel. 24, I
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Pred. No.
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No. 33;
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RESULT 6
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InterPro; IPR000717; PCI.
InterPro; IPR008941; TPR-1ike.
Pfam; PP01399; PCI; 1.
SMART; SM00088; PINT; 1.
SEQUENCE 423 AA; 47909 MW.
Q8D910 PRELI
Q8D910 (TER
01-MAR-2003 (TER
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Uncharacterized of VV12621.
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Q8YZU6;
01-MAR-2002
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01-JUN-2003
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003582; BAB72317.1; -. PIR; AF1851; AF1851. Hypothetical protein; Complete SEQUENCE 248 AA; 27298 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Watanabe A., Iriguchi M., Ishikawa A., Kawashima I Kishida Y., Kohara M., Matsumoto M., Matsuno A., N Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous niti cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical ALR0359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=103690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21595285; PubMed=11759840;
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8; Conserv
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9; Conserv
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L protein Alr0359.
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(TrEMBLrel. 23, Last sequence update)
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lzed conserved protein.
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72.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB
Pred. No. 34;
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                                                                     update)
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ima K., Kimura T.,
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Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                       Matches
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Miyaki C.Y., Furlan L.R., Camargo L.B.A., da Silva A.C.R., Moon D.H.,
Takita M.A., Lemos B.G.M., Machado M.N., Ferro M.I.T., da Silva F.R.,
Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
Coutinho L.L., Kimura B.T., Ferro E.S., Harakava R., Kuramae B.E.,
Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
Leoni S.G., Oliveira A.R., Rosa V.E., Jr., Sassaki F.T., Sena J.A.D.,
de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
Civerolo B.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
Kitajima J.P.,
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01-UN-2003 (TERMBLrel. 24, Lass
01-UN-2003 (TERMBLrel. 24, Lass
01-UN-2003 (TERMBLrel. 24, Lass
Conserved hypothetical protein.
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Vibrionaceae; Vibrio.
NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete SEQUENCE 135 AA; 15769 MW;
                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:1018-1026(2003).
EMBL; AE012557; AA029065.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease and citrus variegated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22421331; PubMed=12533478;
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Xanthomonadaceae; Xylella.
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases
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28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TPTELAKLVNKRSE 14
                                                                           w
                                                                                                                                               Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                           TELAKLVNKRSE 14
TDVAKLVNVRNE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%;
                                                                                                                                                                                  58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chung S.S., Kim J.J., Moon Y.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n Temeculal / ATCC 700964).
Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                   ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                  proteome.
7C540986E7B99455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E2F5F951FA95E132 CRC64;
                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AA.
                                                                                                                                                                              DB
27;
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                                                                                                                                                                                                                          Length 135;
                                                                                                                                                       Indels
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RESULT 9
Q7WL59
ID Q7WL59

PRELIMINARY;

PRT;

162

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Q7W7S
Q7W7S
AC Q7W7S
AC Q7W7S
AC Q7W7S
AC Q7W7S
AC Q7W7S
AC Q7W7S
DF 01-OC

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RX MEDINE-2827954; pubMed=12910271;

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Achtman M., Ackin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Ackin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Ackin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Jordond D., Price C.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Abbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

RA Abbinowitsch E., Rutter S., Sanders M., Saunders D.J.;

RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
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A Parkhill J., Sebalhia M., Freston A., Murphy L.D., Thomson N.,

A Harris D.E.; Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Kabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

A Rabbinowitsch E., Rutter S., Sanders M., Squares R., Squares S., Stevens K.,

A Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

"T Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

Empl. Bx640442; CAB32387:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7WL59;
01-OCT-2003
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
SEQUENCE
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
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Bacteria, Proteobacteria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordetella parapertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BPP2442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7W7S2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transcriptional
                                                               BX640430; CAE37737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
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7; Conserv
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162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPTELAKLVN 10
      proteome
162 AA
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
anscriptional regulator (MarR family).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella.
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      18047 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
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70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulator
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Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB Pred. No. 33; 2; Mismatches
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در
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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      96814512C9198346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nnotation update) (Mark family).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162
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RESULT
Q87440
ID7440
Q8
AC Q8
AC Q8
AC Q8
AC Q8
CO Q9

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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N., A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall J A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A., A Ccrituan M., Atkin R., Baker S., Basham D., Bason N., Cherevach I. A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., A Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K. Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K. A Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price A. Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., A Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steven A. Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Steven T. "Comparative analysis of the genome sequences of Bordetella perture Bordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7VWG8;
Q7VWG8;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                           Q87440;
Q87440;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Tohama I / ATCC BAA-589 / N
MEDLINE=22827254; PubMed=12910271;
                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Envelope glycoprotein (Fragment).
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Alcaligenaceae; Bordetella
                    SEQUENCE FROM N.A.

MEDLINE=95193252; PubMed=7886956;

Rudensey L.M., Kimata J.T., Benveniste R.E., Overbaugh J.;

Rudensey L.M., Kimata J.T., Benveniste R.E., Overbaugh J.;

"Progression to AIDS in macaques is associated with changes in replication, tropism, and cytopathic properties of the simian immunodeficiency virus variant population.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella
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                                                                                                                                                                                                                       Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BX640417; CAE42560.1; -.
  Virology
                                                                                                                                                                                         NCBI_TaxID=11723;
                                                                                                                                                                                                                                           Chimpanzee
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                                                                                                                                                                                                               ee immunodeficiency virus (SIV(cpz)) (CIV)
Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPAELARLIN
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gulator (MarR family).
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RESULT 13
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AC Q8YFH
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DT 01-JU
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OS BRUCE
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COC BRUCE
RESULT 14
QBG2ES
ID QBG2E
AC QBG2E
AC QBG2E
DT 01-WS
DT 01-WS
DT 01-WS
DT 01-WS
DT 01-WS
DT 01-WS
COMBE
GN BROSS
OS Bruce
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Q8YFH4;
01-MAR-2002
01-MAR-2002
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NON TER
SEQUENCE
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STRAIN-16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

manaltenase".
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella. NCBI_TaxID=29461;
                                                                                                                                                                          QBG2E5 PRELIMINARY; PRT; 429 AA.
QBG2E5;
Q1-MAR-2003 (TEMBLrel. 23, Created)
O1-MAR-2003 (TEMBLrel. 23, Last sequence update)
O1-MAR-2003 (TEMBLrel. 23, Last annotation update)
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                                                                                                                            Conserved hypothetical BR0378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. EMBL; AE009590; AAL52729.1; -. PIR; AF3445; AF3445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                   Brucella suis.
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392 AA; 43099 MW;
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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Pred. No. 82;
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome 1 BAC F22H5 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-2801) to the EMBL/GenBank/DDBJ databases.

EMBL; AC025814; AAG12682.1; -.

EMBL; A96783; A96783.

GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPR003866; Isoflav reduct.

Pfam; PF02716; Isoflavone_redu; 1.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete SEQUENCE 429 AA; 47131 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal and plant pathogens and symbionts."; Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Paulsen I.T., Seshadri R., Nelson K.E.,
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mes 8; Conserv
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85
                                                   1 TPTELAKLVNKRS 13
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593 AA; 6
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(TrEMBLrel.)
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97
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                                                                                                                                  Score 40; DB 10;
Pred. No. 1.3e+02;
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56F3752AEA471D1D CRC64;
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Search completed: May 21, 2004, 18:03:09 Job time : 42 secs